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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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JOURNAL PUBMED	TITLE	REFERENCE AUTHORS	SOURCE	ACCESSION VERSION KEYWORDS	RESULT 1 AY032589 LOCUS DEFINITION
Apoptosis Biochem. Biophys. Res. Commun. 284 (1), 77-82 (2001) 11374873	Distribution, P.S. and Bertin, J.  Human CARD12 Is a Novel CED4/Apaf-1 Family Member That Induces	Mammalia: Eutheria; Frimates; Catarrnini; Hominidae; Homo.  1 (bases 1 to 313)  Geddes, B.J., Wang, L., Huang, WJ., Lavellee, M., Manji, G.A.,  Brown M. Turman M. Morgantorn T. Morrism C. Clubernoon	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	CGS. AY032589 AY032589.1 GI:13899172	AY032589 3133 bp mRNA PRI 25-MAY-2001 Homo sapiens caspase recruitment domain protein 12 mRNA, complete

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Bertin, J
Direct Submission
Submitted (15-APR-2001) Neurobiology, Millernium Pharmaceuticals
Inc., 640 Memorial Drive, Cambridge, MA 02139, USA
Location/Qualifiers
1. 3133
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J. Biol. Chem. 276 (30), 28309-28
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Primates;
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t 1200   T 1344	y uyyunya ay uyantica ticayagoctygaacacyytygagaachagototygagyg 	1285	Db 43	
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A 122	5 GTGGTCATCACTTGTGCAATCCAGATGGGTGAAAGTGAGTTCCACTCTCACACACA	16	DЬ	
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C 110	ACAGAAGACAGCGCCCAGGCTCTCATCCGAGAAGTGCTGATCAAGGAGCTTGCTGAAGG	Λ 4		
- 1c 960	1 acagaagacagcgcccaggctctcatccgagaagtgctgatcaaggagcttgctgaagg	90	40	
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9	actgagtgcctgaggcacatacggcagtttggtgccctgactgctgaggtgggggatat	4	Оу	
C 98	5 ATCGAAGCCCTGATAAAGGAAAACCACCGCTTCAAGAACATGGTCATCGTCACCACTAC		Db	
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Stehlik,C., Damiano,J.S., Pio,F.
Direct Submission
Submitted (21-FEB-2001) Program Research, The Burnham Institute,
Jolla, CA 92037, USA
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SKSALSQEFEAFFQKSLYINSGNIPDYLFDFFEHLPWCASALDFIKLDFYGGAMASW
EKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDESKLNKODIRYLGK
IFSSATSLRLQIKRCAGYAGSLSIVLSYCKNIXSLMVEASPLTIEDESKHTSVYNLKT
LSIHDLQNQRLDEGGLTDSLGNIKNLTKLIMDNIKMNEEDAKILAQNLHNLVKLSILDLS
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≨ — a	ggtaaaagcttattatcaactcagggaacatccccgattacttatttgacttctttga 	1741 2230	Qу Дъ	
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               The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 160583)
                                                Waterston, R.H.
                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 160583)
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11 unordered pieces.
AC010968
AC010968.5 GI:9845170
HTGS_PHASE1; HTGS_DRAFT.
                                                                                                Homo sapiens
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2 clone
                                                                       Catarrhini;
                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                     RP11-9302,
                                                                        Hominidae;
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Center code: WUGSC
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Insert size: 159583; sum-of-contigs
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Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
2000 this sequence version replaced gi:8439959
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Sequencing vector: plasmid; 418
Chemistry: Dye-primer ET; 478 of reads
Chemistry: Dye-terminator Hig Dye; 538 of
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least 030
Consensus quality: bases at least 030
Consensus quality: bases at least 030 Quality coverage: 6.64 in Q20 bases; agarose-fp Quality coverage: 6.38 in Q20 bases; sum-of-contigs Web site:http://genome.wustl.edu/gsc/index.shtml NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. Summary Statistics ----and the accession number bp in length Sequencing reads

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BASE COUNT
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                                         CTCAGGGAACATCCCCGATTACTTATTTGACTTCTTTGAACATTTGCCCCAATTGTGCAAG
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                                              CTTGTACCATACCCCATCTTTTCTGAACTTTTATCCCCCTTGGTGAAGATATTGACATTAT
                                                                                          cttgtaccataccccatcttttctgaacttttatccccttggtgaagatattgacattat
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Weissenbach, J.

Spastin, a novel AAA protein, is altered of autosomal dominant spastic paraplegia Nat. Genet. (1999) In press

'hases 1 to 138909)
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Direct Submission

Submitted (29-FEB-2000) to the EMBL/GenBank/DDBJ databases

On Mar 6, 2000 this sequence version replaced g1:6002386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete sequence. AL121653 GI:715
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                                                                                                                                                                                                                  GGAGTACACAGCAGGACGAAGACTCAGCAGTTTATTGACGTCTCATGAGCCAGAGGAGGT
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RESULT 7
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Homo sapiens mRNA full

AL38934.1 GI:9367839

FLI_CDNA.

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Pluvinet, R., Estivill, X.,
                                                       Auffray, C., Ansorge, W., Ballabio, A., Estivill, X., Gibs, n, K., Lehrach, H., Poustka, A. and Lundeberg, J.

The European IMAGE consortium for integrated Molecular analy human gene transcripts
Unpublished
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 99.9
Matches 1317; Conservative
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Direct Submission

AL Submitted (15-JUL-2000) Dept. Genetica Molecular, Institut de Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. Gran via SpAIN. Tel: ++14-93-260-7775 Fax: ++34-93-260-7776 WMW site: http://www.iro.es e-mail enquiries: lsumoy@iro.es CUNS URP 420 - Genetique Moleculaire et Biologie du Developement J4801 Villejuif Cedex, FRANCE Fax: ++34-93-260-7776 WWW site: EURO-IMAGE Consortium Contact: Auffray C IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8

FR 1221 - Rue Guy Moquet 19, Batiment G - BP 8

FRA: ++33-1-49 58 34 98

FRA: ++33-1-49 58 34 98

FRA: ++33-1-49 58 35 09

e-mail: auffray@infobiogen.fr
This clone is available royalty-free through IMAGE Consortium Distributors.

IMPORTANY: This sequence represents the full insert of this IMAGE CONVA clone. No attempt has been made to verify whether this was derived.
                                                                                                                                                                                                                                                   tgcaagtgctctggacttcattaaactggacttttatgggggagctatggcttcatggga 1874
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JOURNAL REFERENCE AUTHORS

2114

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REFERENCE AUTHORS

TITLE

VERSION KEYWORDS SOURCE ORGANISM

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Mammalla; Eutheria; Primates; Catt
1 (bases 1 to 1395)
Damiano, J.S., Stehlik, C., Pio, F.,
Clan, a novel human ced-4-like ger
Genomics. 75 (1-3), 77-83 (2001)
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ARLVGWGPDDDDLSVITGAFKLVTA"
a 248 c 327 g 384 t
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277. .1356
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/tissue_type="lung"
1. .1395
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Damiano, J.
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95.9%;
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Pred. No. 5.2e
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.2e-208;
les 36;
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                                                                                                                                                              2 (bases 1 to 768)
Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.
Direct Submission
Submitted (21-FEB-2001) Program on Apoptosis and Cell:
Submitted (21-FEB-2001) Program on Apoptosis and Cell:
Research, The Burnham Institute, 10901 North Torrey Pi
Jolla, CA 92037, USA
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 768)
Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C. Clan, a novel human ced-4-like gene Genomics. 75 (1-3), 77-83 (2001)
                                                                                                                                                                                                                                                                                                     human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                       AY027789 768 bp mRNA
Homo sapiens CLANC (CLAN1) mRNA,
AY027789
AY027789.1 GI:14324116
                                                                                                                                                                                                                           11472070
/product-"CLANC"
/protein_id-"AAK1478.1"
/db_xref="Gi:14324117"
/translation-"MNFIKDNSRALIQRMGMTVIKQITDDLFVWN'/LNREEVNIICCE
                                                            /gene="CLAN1"
277. .747
                                                                                 /map="2p22-p21"
/tissue_type="lung"
1. .768
                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                                  Location/Qualifiers
                                         /codon_start=1
                                                  /gene="CLAN1"
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complete cds
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Torrey Pines R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 185281)
Waterston, R.H.
Direct Submission
Submitted (04-OCT-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Mar 10, 2001 this second
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 185281)
Waterston, R. H.
The sequence of Homo sapiens clone
Unpublished
                                                                                                                                                                                                                                                                                                       AC011232 185281 bp
Homo sapiens chromosome
7 unordered pieces.
                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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AC011232.7 GI:13270720
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QDLKDLYHTPSFLNFYPLGEDIDIIFNLKSTFTEPVLWRKDQHHHRVEQLTLVL"
a 157 c 180 g 213 t
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Pred. No.
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2 clone RP11-78E13,
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9.7e-113;
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WORKING DRAFT SEQUENCE,
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Db 185281 GAATTCAGGACTCTGGAGGTCACACTCCGGGATTTCAGCAAGTTGAATAAGCAAGATATC 185222
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Best Local Similarity
Matches 324; Conserv
                                                                    185221 AGATATCTGGGGAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGT
                                                                                                                                                                                   1972 gaattcaggactctggaggtcacactccgggatttcagccaagttgaataagcaagatatc 2031
                                                                                              2032 acatatctggggaaaatattcagctctgccacaagcctcaggctgcaaataaagagatgt 2091
2092 gctggtgtggctggaagcctcagtttggtcctcagcacctgtaagaacatttattctctc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 168000; agarose-fp
Insert size: 184681; sum-of-contigs
Quality coverage: 7.07 in Q20 bases; agarose-fp
Quality coverage: 7.33 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                             52719
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                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig17"
36957 c 37187 g 57816 t
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112232. .185281
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69283. .112131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig14"
41547. .69182 .
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8284. .22741
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2086. .8183
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/db_xref="taxon:9606"
/chromosome="2"
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2085: gap of unknown length
8183: contig of 6098 bp in length
8283: gap of unknown length
22741: contig of 14458 bp in length
22841: gap of unknown length
41446: contig of 18605 bp in length
41546: gap of unknown length
69182: contig of 27636 bp in length
69282: gap of unknown length
121213: contig of 42849 bp in length
112231: gap of unknown length
112231: gap of unknown length
1185281: contig of 73050 bp in length
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Pred. No. 5.5e-67;
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tcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaatcttaagcaatt 2900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS01DS8 162692 bp DNA 02-MAR-2000 BAC sequence from the SPG4 candidate region at 2p21-2p22 BAC 563N04 of RPCI-11 library from chromosome 2 of Homo sapiens (Human),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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t. Genet. (1999) In press
(bases 1 to 162692)
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32017 c 32887 g
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Stehlik.C., Damiano,J.S., Pio,F., Godzik,A. and Reed,...C.
Direct Submission
Submitted (21-FEB-2001) Program on Apoptosis and Cell Des
Submitted (21-FEB-1001) Program on Apoptosis and Cell Des
Research, The Burnham Institute, 10901 North Torrey Pines
Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Entel Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 578)
Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reed, .f.C. Clan, a novel human ced-4-like gene Genomics. 75 (1-3), 77-83 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AY027790 S78 bp mRNA PH
HOMO Sapiens CLAND (CLAN1) mRNA, complete
AY027790
AY027790.1 GI:14324118
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                                                                                                                                                                                                                 8.8%; Score 269; DE ilarity 100.0%; Pred. No. 4e-Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                               /codon_start=1
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106 c 143 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CLAN1"
277. .555
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="2p22-p21"
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1. .578
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                                                                                                                                                                                                                                                                                                                                                                                           /note="CARD protein"
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="CLAN1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                             Score 269; DB 9;
Pred. No. 4e-61;
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10901 North Torrey Pines Road, La
                                                                                                                                                                                                                  0;
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e cds.
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2615 tcgacaggatgaacgtgctagaacagctcaccgcactgatgctgccctgggggctgtgacg
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primer_bind
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Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Michael Olivier, David R. Cox Stanford Human Genome Center Stanford University School of Medicine 4005 Miranda Ave. 2nd Fl., Palo Alto, CA Tel: (650) 320-5800
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu primer A: AATAAGGGGGCAAAATAAGCAAA Primer B: TAACACCCCTTTGTTCTTCCTCA STS Size: 322
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 553)
Olivier,M. and Cox.D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)
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SHGC-100923 Human Homo
G55568 G55568.1 GI:6120887
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and
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developed at the Stanford Human
Location/Qualifiers
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ilarity 100.0%;
Conservative (
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KCl:
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AmpliTaq Gold Polymerase:
Total Vol:
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Polymerization:
PCR Cycles:
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Denaturation:
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                                                                              complement(304..326)
a 107 c 114 g
                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="2"
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5. .326
   0;
Score 170; DB 11;
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   Gaps
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/gene_"Malp6" /gene_"Malp6" /gene_"Malp6" /gene_"Malp6" /gene_"neuronal apoptosis inhibitory protein 6 /groduct="neuronal apoptosis inhibitory protein 6 /product="neuronal apoptosis protein 6 /product="n	11,137921393,1215521374,23371,2014220241.2125533453)) 71,2014220241.2125633453)) 86,3233732436,3288633453)	/gene="Naip" 4"  gene "Naip" 4"  /product="neptroja" 4"  /gene="Naip" 4"	mRNA 11639 1791, 13792 120241,21255 21377,34514 34589) 11639 19171,20142 20241,21256 33577,34514 34589) 19090 19171,20142 32436,32866 33577,34514 51 25105 25186,32337 32436,32867 protein 6"	/chromosome=m13" /chromosome=m167" /clone="makC 26f17" /clone=makC 26f17" /note==centromere proximal sequence fragment /note==centromere proximal sequence fragment	FEATURES 1. 11791 Source /organism="Mus musculus" -organism="Auxon:10090"	Direct Submission (198-MAR-2000) Genetics, Submitted (08-MAR-2000) MA 02115 Submitted (08-MAR-2000) Malifiers				X S	AF242431 AF242431.1 GI:9082148	Wis musculus neuronal Aus musculus neuronal Nai	RESULT 14 ROD REPLACE (MAIPS) gene, PESULT 14 ROD ROD PROPERTY PRO	TTGGGTTGAAAAACTGGAGACTCA	258 TCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTAGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGCTAGAACAGCTCACCGCACTGATGCACCGCACAGCCCTCAACCCTCAACCCTCAACCACACCTCTCAACCACCA	Tue Mar 26 11:36:43 2002
exon	exon	exon	exon	STS	exon	STS	exon		exon	STS	STS	STS	STS	STS		
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AESLOATVSSCGQLALTGLESSCREENSDDLAEAGYDEDVKLTTFLMSKETAGRLRPV
RELGPLEQEELAAVRLTELLSDRAGEDDLGLYVLROIDSPLKAINSENIFLYVYSS
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KSSKAAPTVVSHLLOLVDEKESLENMSBREDYKKLHOOTELMEGGWAGGLMLVSPESF
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SEPVSEHLLRLALIFAXESMYVAECSPFILOFLAGENGVLAUVLMEVFEASGSI
SEVSEHLLRLSVYPTSEKROPPALINEESFANTENSELSLSKASGSI
RSLKVSTIKONKMSSYDNYSKESPKESFANTENSELLSKADGELLTLAALGSLEVSETN
RSLKVSTIKONKMSSYDNYSKASTENDEFINITENSGCELAMTFANILD
EFHLENSSGFLESIRPALELSKASVTKOSMSRLELSRADGELLTLAALGSLEXVATULOU
EFHLENSSGFLESIRPALELSKASVTKOSMSRLELSRADGELLTLAALGSLEXKATRLEESGGCEAMTFANILD
LLPOLEHNLHKFIGLKELGVLAGELKINILELLYPTGDGIHQVAKLIVRQCLOL
OLPDOLEHNLHKFIGLKELGESLMTALASCKKLEEIERSGGCEAMTFANILT
LVKETONFPNILDESSYIEIGEKFAOALGSLRNILELLYPTGDGIHQVAKLIVRQCLOL
FVSLKILSLKGGOFADKETSEKFAOALGSLRNILELLYPTGDGIHQVAKLIVRGCLOL
FVSLKILSLKGGOFADKETSEKFAOALGSLRNILELLYPTGDGIHQVAKLIVRGCLOL
FVSLKALSHOLDEDMKVINDVK
FVSLKALSHOLDENTFORGREYFAOALGSLRNILESGTRLOMLSWLLDEEDMKVINDVK
FCLRVLAGCHOLDENTFORGREYFAOALGSLCNILDISMNIKITEEGTREDDKKVINDVK
FOLRVLAGCHOLDENTFORGREYFAOALGSLCNILDISMNIKITEEGTREDDKKVINDVK
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 4752)
Huang,S., Scharf,J.M., Growney,J.D., Endrizzi,M.G. and Dietrich,W.F.
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Sequence 2, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	•	Sequence 28, Appl	Sequence 28, Appl	-		Sequence 107, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli

## ALIGNMENTS

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Matches 226;
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CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1232
TYPE: PRT
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TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477,139914
                                                                                                                                                                                                                                                                                                                                                                     344 FLQNMKS-SAEVTPDLQSRGELCELLETTSESNLEDSIAVGPIVPEMAQGEAQWFQEAKN 402
                                                                                                                                                                                                                                                                                                                         101 LAQDLKDLYHTPSFLNF------YPLGEDIDIIFNLKSTFTEPVLWRKDQHHHR 148
                                                                                                                                                                                                                                                                                                                                                                                                                69 FLKSLKEWNYPLFQDLNGQ----SLFHQTSEGDLDD-------
                                           IKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKELA--EGLL 322
                                                                                                                                                                                                             VEQLTLNGLLQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLS--
IQKNHLSRTCLLIAVRTNRARDIRRYLETILEIQAFPFYNTVCILRKLFSHNMTRLRKFM
                                                                                                                                    RAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEF - - KPQNCPEIEAL
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Pred. No. 4.2e-42;
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ASDFIR-SLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTA 2RFKPKY 439

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Matches

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Sequence 23, Application US/08836134A
Patent No. 6020127
Patent No. 6020127
Patent Information:
APPLICANT: Mackenzie, Alex E.
APPLICANT: Mackenzie, Alex E.
APPLICANT: Mackenzie, Mobert G.
APPLICANT: Macken, Main S.
APPLICANT: Roy, Natalie
APPLICANT: Roy, Natalie
APPLICANT: Roy, Natalie
APPLICANT: Roy, Natalie
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and Patent No. 6020127
PITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and Patent No. 6020127
UTILE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and Patent No. 4020127
UTILE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and Patent No. 1020127
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UTILE OF INVENTION: Neuro
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                                                                     NDIDVVGQDMLEILMTVFSASQRIELHLNHSRGFIESIRPALELSKASVTKCSISKLELS
                                                                                                                                                                                                                                         YLFD-----FFEHLPNC--ASALDFIKLDFYGG--AMASWE 625
                                                                                                                                                                                                                                                                             PSTKAGPKIVSHLLHLVDN------KESLENISENDDYLKHQPEISLQMQL
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                                                                                                     RDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCK-NIYSLMVEASPLT 725
                                                                                                                                     RNLAEKEDNVKSYMDMQRRASPDLSTGYWKLSPKQYKIP------CLEVDV 1015
                                                                                                                                                                                                         YFFDHPESLSLLRSIHFSIRGNKTSPRAHFSVLETCFDKSQVPTIDQDYASAFEPMNEWE 970
                                                                                                                                                                                                                                                                                                               LKAI----NINSFVECGIHL-----YQESTSKSALSQEFEAFFQGKSLYINSGNIPD
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RESULT
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US-09-180-439-3
US-09-180-439-3
Sequence 3, Application US/09180439
Patent No. 6225532
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance gen
CURRENT FALLING DATE: 1999-12-06
CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT APPLICATION NUMBER: PCT/GB97/01249
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FILE REFERENCE: 620 - 53
CUBRENT APPLICATION NUMBER: 05/09/180,439
CUBRENT FILING DATE: 198-12-06
EARLIER FILING DATE: 1997-05-08
EARLIER FILING DATE: 1996-05-09
EARLIER FILING DATE: 1996-05-09
EARLIER FILING DATE: 1996-09-24
EARLIER FILING DATE: 1996-09
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Query Match initiatity 23.0%; pred. No. 1.2e-06;
Best Local Similarity 23.0%; Mismatches 208;
Matches 147; Conservative 108; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 YNNKLSG--SIPEEIGYLRSLTYLDLGENALNGSIPASLGNL----NNLFMLYLYNNOL 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 SKLNKODITYLGKIESSATSLRLOIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLT---I 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 SGSIPEEIGYL----SKLTELYLGNN---SLNGSIPASLGNLNNLEMLYLYNNOLSGSIP 448
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                                                                                                                                                                                                                                                                                                                                          501 NMRNLOTE-----FLSDNDLIGEIPSFVCNLTSLEVLYMSRNNLKGKVPQCLGNISDLH 554
                                                                                                                                                                                                                                                                                                                                                                                 787 -LKNLKKMCLFHLTHLSD---IGEGMDYIVKSLSSE------PC--DLEEIQ 826
                                                                                                                                                                                                                                                                                             827 LYSCCLSANAVK-ILAQNLHNLVKLSILDLSENYLEKD-----GNEALHELIDRMNVLEQ 880
                                                                                                                                                                                                                                                      555 ILS--MSSNSFRGELPSSISNLTSLKILDFGRNNLEGAIPQFFGNISSLQVFDMQN--NK 610
                                                                                                                                                                                                         881 LTAIMLEWGCDVQGSLSSLLKH----LEEVP------QLVKLGLKNWRLTDT------ 922
                                                                                                                     923 --EIRILGAFFGK--NPLK------NFQQLNLAGNRVSSDGWLAFMGVFENLKQLVF 969
                                 970 FDFSTKE----FLPDPALV-----RKLSQVLSKLTFL 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDERHITSVTNLKTLSIHDLONQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEG 786
                                                                                                                                                                     LSG-TLPTNESIGCSLISLNLHGNELADEIPRSIDNCKKLOVLDLGDNOLNDTEPMWIGT 669
                                                                                 LPELRVLRLTSNKLHGPIRSSGAEIMFPDLRIIDLSRNAFSOD---LPTSLFEHLKGMRT 726
VDKTMEBPSYESYYDDSVVVVTKGLELEIVRILSLYTII 765
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Sequence 2, Application US/08930996A patent No. 6100449 patent No. 1NFORMATION: GENERAL INFORMATION: FLUHR, Robert APPLICANT: FLUHR, Robert RESULT 5 US-08-930-996A-2

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FILING DATE: 13-APR-1995
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
; TYPE: amino acid
; TYPE: maino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-930-996A-2
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3.2%; Score 170.5; DB 3;
Best Local Similarity 19.8%; Pred. No. 2.4e-06;
Matches 231; Conservative 160; Mismatches 393;
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MEDIUM TYPE: Floopy disk

MEDIUM TYPE: Floopy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATCHOILD DATA:

APPLICATION NUMBER: US/08/930,996A

FILING DATE: 09-DEC-1997

PRIOR APPLICATION DATA:

THING DATE: 13-APR-1996

PRIOR APPLICATION DATA:

APPL
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APPLICANT:
APPLICANT:
APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BOOMY AND NEIMARK
STREET: 419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE TITLE OF INVENTION: LOCUS OF TOWATO AND USE THEREDE FOR TRANSFORMATION AND TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 PSFLNFYPLG----EDIDIIFNLKSTFTEPVLWRKD-QHHHRVEQL-----T.NGL--- 157
              574
                                                                      372 QKNKHKHKGVAASDFIRSLDHC-----GDLALEGVFSHKFDFELQDVSSVNEDVL----
                                                                                                                               515 HCIRLEDNKGSHMLEQCRHMSYSIGQDGEFEKLKSLFKSEQLRTLLPIDIQFH-YSI:KLS 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 KGLLQEIGSTDLK++ADD-----NLNQLQVKLKADDNLNQ------LQV.(LKEKLNG 285
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CITY: Washington
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LFLKSLKE-W--NYPLFQDLNGQSLFHQTSEGDLDD------LAQLLKDLYHT 111
          KRVLHNILPTLRSLRALSLSHYQIEVLPNDLFIKLKLLRFLDLSETSITKLPDSIFVLYN
                                                                                                                                                                                                                                                                                                                                                                                                                                  DQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFKPQNCPEIEALIKENHRF-KNMVI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKALAGMLRSKSEVDEWRNILRSEI---WELPSC------SNG::LPALM 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGG:FETLC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----MGILSSEDSWALFKRHS-----LEHKDPKEHPEFEEVGKQIADK(KGLPLA 384
                                                                                                                                                                                            RCLRNLMKTPLFVVITCAI-----QMGESE-----FHSHTQTTL-----FHTFY)LLI 371
                                                                                                                                                                                                                                                        HLWIANGLVH--QFHSGNQYFIELRSRSLFEMASEPSERDVEEFLMHDLVNDLAQIASSN
                                                                                                                                                                                                                                                                                                                 VTTTTECLRHIRQFGA------LTAEVGDMTEDSAQALIREVLIKELAEGLLL()IQKS 328
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ZAMIR, Daniel
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                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-09-353-585-2
(Sequence 2, Application US/09353585
; Patent No. 6287865
; Patent No. 6287865
; GENERAL INFORMATION:
Jones, David A
Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon & Vanderhye PC
ADDRESSE: Nixon & Vanderhye PC
ASTREET: 8th Floor, 1100 no. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 2201-4714
COMPUTER READABLE FOORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             819
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                                                                                                                                                HLKS-LTSLQFLRIVGNLSQFQSQGQLSSFSHLTSLQTLQIWNFLNLQSLPESALPSSLS
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                                                                            Q-VLSKLTFLQEARLVGWQFDDDDLSV 1014
                                                                                                                                                                                                                                 FGKNPLKNFQQLNLAGN--RVSSDGWLAFMGVFENLKQLVFFDFSTKEFLPDPALVRKLS 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PELLPSIKELRLTYC-----PEIEGELPFN---LQILDI--RYCKKLVNGRKEWH---- 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLTKLIMDNIKMNEEDAIKLAEGLKNLKKMCL----FHLTHLSDIGEGMDYIVKSLSSE 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILPTTLKRIKISGCPKLKLEAPVGEMFVEYLSVIDCGCVDDISPEFLPTARQLSIENCH 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EASPLTIE------DERHITSVTNLKTLSIHDLQNQRLPGGLTDSLGNLK 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTTGLL--CKYTAQRFKPKYKFFHKSFQEYTAGRRLS--SLLTSHEPEEVTKGNGYL---
                                                                                                                                                                                                                                                                                                                        ----LQRLTELWIKHDGSD------EHIEHWELPSSIQ------RLFIFNLKTLSSQ 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P---CDLEEIQLYSCCLSANAYKILAQNLHNLYKLSILDLSENYLEK--DGNEALHELID 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVTRFLIPTATESLH------IRNCEKLSMACGGAAQLTSLNIWG-----CKKLKCL 1014
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Best Local Similarity
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                                        859 YLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWR 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MS MARY J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 62/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
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AL----NGSIPASFGNLNNLSRLNL------VNNQLSGSIP--EEIGYLRSLNVLD--
                                                                                                                                                                                                    GNLKNLTKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHLSDIGEGMDYIVK----SL 815
                                                                                                                                                                                                                                              --GSIPASLGNLKNLSRLNLVNNQLSGSIP---ASLGNLNNLSMLYLYNNQLSGSIPASL
                                                                                                                                                                                                                                                                                     VAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKTLSIHDLQNQRLPGGLTDSL 759
                                                                                                                                                                                                                                                                                                                               ---YL------RSLNVLGLSENALN-----
                                                                                                                                                                                                                                                                                                                                                                    PETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAG 699
                                                                                                                                                                                                                                                                                                                                                                                                            EICYLRSLTYLDLSENALNGSIPASLGNLNNLSFLFLYGNQLSG--SIPEEIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFLS-----PEEISYLRSLTELD 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWRQESLQSVKNTTEQE 544
                                                                              SNNSINGFIPASFGNMSNLAFLFLYENQLASS------VPEEIGYLRSLNVLDLSEN
                                                                                                                                                             GNLNNLSMLYLYNNQLSGSIPASLG-NLNNLSRLYLYNNQLSGSIPEEIGYLSSLTYLDL 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN: Cf2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 816-400 TELEFAX: (703) 816-4100
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                                                                                                                     -LEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSEN
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Pred. No. 6.6e-06;
Nismatches 199
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-353-585-3
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US-09-33-585-3
; Sequence 3, Application US/09353585
; Patent No. 6287865
; GENERAL INFORMATION:
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                                                        Query Match
Best Local Similarity
Matches 139; Conserv
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425 GLLCKYTAQRFKPKYKFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDIT 484
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dixon,
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
COUNTRY: United States
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/353,585 FILING DATE: 15-Jul-1999 CLASSIFICATION: C12N 15/29, 15/82,
                                                                                                                                                                                           ORGANISM: Tomato STRAIN: Cf2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ms Mary J Wilson REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/930,277 FILING DATE: 27-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon & Vanderhye STREET: 8th Floor, 1100 No.
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                                                          Conservative
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                                                        81;
                                                    Score 165; DB 4; I
Pred. No. 6.6e-06;
1; Mismatches 199;
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6287865th Glebe Road
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                                                                                        Length 1112;
                                                        Indels 224;
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Sequence 8. Application US/09180439

Patent No. 6225532

Patent No. 6225532

APPLICANT: Dixon, Mark S
APPLICANT: Hatzixanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, David A
APPLICANT: Jones, David A
COURENT APPLICATION NUMBER: US/09/180,439

EARLIER APPLICATION NUMBER: US/09/180,439

EARLIER FILING DATE: 1998-12-06

EARLIER APPLICATION NUMBER: PCT/GB97/01249

EARLIER FILING DATE: 1997-05-08

EARLIER APPLICATION NUMBER: GB 9609681.3

EARLIER FILING DATE: 1996-09-24

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 1016
                                                             ; ORGANISM: Lycopersicon esculentum US-09-180-439-8
       Query Match
Best Local Similarity
                                                                                                  LENGTH: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     592 PASLGNLNNLSMLYLYNNQLSGSIPEEI-----GYLSSLTYL 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   534 LSENALNGSIPASFON--LNNLSRLNLVNNOLSGSIPEEIGYLRSLNDLGLSEN.LNGSI 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               919 LTDTEIR-ILGAFFGKNPLKNFQQLNLAGNRVSSD-----GWL------------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           490 AL----NGSIPASFGNLNNLSRLNL------VNNOLSGSIP--EEIGYLRSL NVLD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     859 YLEKDGNEALHELIDRMNYLEQLTALMLPWGCDYQGSLSSLLKHLEEYPQLYKL:3LKNWR 918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 --GSIPASLGNLKNLSRLNLVNNQLSGSIP---ASLGNLNNLSMLYLYNNQLS:SIPASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 ---YL-----FDFFEHLPN---CASALDFTKLDF---YGGAMASWEKAAEDT¢GIHMEEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWRQESLQS/KNTTEQE
       3.1%;
22.1%;
Score 164; DB 4;
Pred. No. 7e-06;
        Length 1016;
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US-08-353-700-1
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                                               STREET: LOUL ....
CITY: PHILADELPHIA
STATE: PA
TCA
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Sequence 1, Application US/08353700

Patent No. 5599919

GENERAL INFORMATION:
APPLICANT: YEN, TIMOTHY J.
APPLICANT: YEN, TIMOTHY J.
TITLE OF INVENTION: NUCLEIC ACID ENCODING A
TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN,
UNDRER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: 1601 MARKET STREET, SUITE 720

CTTY. BHILARRIDHYA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            943 NLAGNRVSSDGWLAFMGVFENLKQLVFFDFSTKE-----FLPDPALV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               691 LDNCKKLOVLDLGDNOLNOTFPMWLGTLPELRVLRLTSNKLHGPTRSSGAEIMFPDLRII 750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              634 NLEGAIPOFFGNISSLOVFDMON--NKLSG-TLPTNFSIGGSLISLNLHGNELADEIPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 859 YLEKD-----GNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKH-----LEEVP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           576 SLEVLYMSRNNLKGKVPOCLGNISDLHILS--MSSNSFRGELPSSISNLTSLKILDEGRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643 YIPSRAVSLFENWKOEFRTLEVTLRDESKLNKQDITYLGKIFSSATSLRLQIKRCAGVAG
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JS-08-353-700-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3248 amino aci
     1207
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                                                                                                                                                  1111 RSEMTDNONNSKSEAGGLKOEIMTLKEEQNKMOKEVNDLLOEN-----EQLMKVMK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: REED, JANET E.
                                                                                                                                                                                                                                                                                                    993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.8%; Score 149.5; DB Local Similarity 18.4%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
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 NAQLVQLEAMLRNKELKLQES---
                                                                                                                                                                                   SSLLTSHEPEEVTKGNGYLQKMVSISD----ITSTYSSLLRYTCGSSVEATRAVMKHLAA 511
                                                                                                                                                                                                                        SKLECLLNECTSLCENRKNELEQLKEAFAKEHQEFLTKLAFAEERNQNLMLELETVQQAL 1110
                                                                                                                                                                                                                                                                                                LIQKSESFANYIDEREKSISELSDQYKQEKLILLQRCEETGNAYEDL-SQKYK-AAQEKN 1050
                                                                                                                                                                                                                                                                                                                                   LIQKNK-----HKHKGVA-ASDFIRS-----LDHCGDL--ALEGVFSHKFDFELQDVS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                QRISKLQEDTSAHQN-VVAETLSALENKEKELQLLNDKV----ETEQAEIQELKKSNHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIICCEKVEQDAARGIIHMILKKGSESC------NLFLKSLKEWNYPLFQDLNGQ--
                                   SALSQEFEAFFQGKSLYINSGNIPDYLFDFFEHLPNCAS-ALDFIKLDFYGGAMASWEKA 627
                                                                                                           VYQHGCLLGLSIAKRPLWRQESLQS--VKNTTEQEILKAININSFVECGIHLYQES-TSK 568
                                                                                                                                                                                                                                                             SVNEDVLLTTGLLCKYTAQRFKPKYKFFHKSFQEY-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EFSLESQKQMNSDLQKQCEELVQIKGEIEEN-----LMKAEQM------HQSFVAETS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEIEALIKENHREKNMVIVTTTTECLRHIRQEGALTAEVGDMTEDSAQALIREV-LIKEL
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                                                                          -QNLESEPIRNSVKERESERNQCNFKPQMDLEVKEISLDSY
-EKEKECLQHELQTIRGDLETSNLQDMQ--
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RESULT 10
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GENERAL INFORMATION:
APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
TITLE OF INVENTION: Nucleic Acid in TITLE OF INVENTION: Expressed Kine
                  TELEFAX: (215) 563-4044 INFORMATION FOR SEQ ID NO:
                                                    ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1615
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                  APPLICATION NUMBER: US 08/353,700 FILING DATE: 09-DEC-1995
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acid Encoding 
Expressed Kinetochore
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Protein, and
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LENGTH: 3248 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
PCT-US95-16216-1
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                                                                                                                                                                                                                                                                                                                     1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1051 SKLECTLNECTSICENRKNELEQLKEAFAKEHQEFLTKLAFAEERNQNLMLELETVQQAL 1110
1435 LQTYVDSLKAENLVLSTNLRNFQGDLVKEMQLGLEEGLVPSLSSSCVPDSSSLSSLGDSS 1494
                                                                                                                                                                                                             1315 YELVTELNDSRSECITATRKMAEEVGKLLNEVKILNDDSGLLHGELVEDIPGGEFGEQPN 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 WRKDQHHHRVEQLTLNGLLQALQSPCIIEGESGKGKSTLLQ-RIAMLWGSGICKALTKFK 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 NIICCEKVEQDAARGIIHMILKKGSESC------NLFLKSLKEWNYPIFQDLNGQ-- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVNEDVLLTTGLLCKYTAQREKPKYKEFHKSEQEY-----TAGRRL 455
                                              FSSATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPL----TIED------ 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEIEALIKENHREKNMVIVTTTTECLRHIRQEGALTAEVGDMTEDSAQALIRIV-LIKEL 317
                                                                                                  EQHPVSLAPLDESNSYEHLTLSDKEVQMHFAELQEKFLSLQSEHKILHDQHCQMSSI:MSE 143
                                                                                                                                                ERHITSVTNL-----KTLSIHDLQNQRLPGGLTDSLGNLKNLTKLIMD------
                                                                                                                                                                                                                                                                                                               SQEISGLKDCEIDAEEKYISGPHELSTSQNDNAHLQCSLQTTMNKLNELEKICEIIQAEK 1314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSLLTSHEPEEVTKGNGYLQKMVSISD----ITSTYSSLLRYTCGSSVEATRAV KHLAA 511
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C	Db RESI US Pr	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	)
We Embarcadero Center, Eighth Floor Ifornia USA 1-3834 1-3834 IBM PC Compatible SYSTEM PC COMPATIBLE E: Floppy disk IBM PC COMPATIBLE SYSTEM PC COMPATIBLE OP-OCT-1997 PATENTIN RAPAS E: 09-OCT-1997 ATION DATA: N NUMBER: PCT/US97/18802 ATION DATA: 10-OCT-1997 ATION DATA: 10-OCT-1997 ATION DATA: CON NUMBER: PCT/US97/18802 OP-OCT-1997 ATION DATA: 10-OCT-1997 ATION DATA: CON NUMBER: 023070-070210US ATION INFORMATION: Lian, Kevin L. ON NUMBER: 023070-070210US ATION INFORMATION: (415) 576-0300 (415) 576-0300 (415) 576-0300 (415) 576-0300 R SEQ ID NO: 3: RACTERISTICS: 255 amino acids 10 acid 11 near	947823  lerie M.  ouhi r  hen dures and Mate dures and Mate	809 DY	OO DVTUVGI SCHOOL STANKE STOOL S

Tue Mar 26 11:36:23 2002

RESULT 12439-6 polication US/09180439 US-09-ance 6, Application US/09180439 Sevent No. 622523N. SERVILLE NO. 62252N. SERVILLE NO. 622523N. SERVILLE NO. 622523N. SERVILLE NO. 62252N. SERVILLE NO. 62252N	Db 1007 CSFFDMDADESILIAEDTKLENLRILTELLISYSKDTKNIFKFFPNLLSFELKESWDY 1066  Db 1007 CSFFDMDADESILIAEDTKLENLRILTDTEIRILGAFFGKN 934  891 DVGGSLSSLLKHLEEVPOLVKLGLKNWRLTD

Page 10

TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 496-88224
INFORMATION: (617) 876-88224
SEQUENCE CHARACTERISTICS: 4:
TYPE: 661 anio acids
TYPE: 1 inear
TOPOLOGY: 1 inear
US-08-514-014-4 ATTORNEY/AGENT INFORMATION: RESULT 13 US-08-514-014-4 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATER: LBM PC COMPATER:
CURRATING SYSTEM: PC-DOS/MS-DOS
APPLICATION DATA: Relos/MS-DOS
APPLICATION DATA: US/08/514,014 equence 4 CORRESPONDENCE ADDRESS: 12

CORRESPONDENCE ADDRESS: 12

STREED: 87 Cambridge Father Street: 187 Cambridge Father Street: 187 Cambridge Father Street: 187 Cambridge Father Street: 187 Cambridge Father Street: 188 Cambrid STRATION NUMBER: 32,724
SRENCE/DOCKET NUMBER: GI UNTRY: Wassachusetts INFORMATION: Application US/08514014 Jacobs, Kenneth McCoy, John Laher, Kerry
Lin, McKeough
CON: DNA SEQUENCES AND SECRETED PRITEINS
CON: ENCODED THEREBY GI6000

δÔ ę.yo Ъ Qγ Дb VΩ DЬ Qy DЬ Qy 793 LAEGLKNIKKMCLFHLTHLSDIGEGMDYIVKSLSSEPC-DLEETOLVSCCLSANAVKILA 841 341 AANFPSLTHLYIRGNVKKL------HLGVGCLEKLGNLQTLD---LSHNDIEASICCS 389 723 PLTIEDERHITSVTNLKTLSIHDLONORLPGGLTDSLGNLKNLTKLIMDNIKNNEEDAIK 782 283 EHRESDISSTTFOCFTQLQELDLTATHLKGLPSGMKGLNLLKKLVLSV--NHFDQICQIS 340 Query Match
Best Local Similarity 2:7%; Score 142; DB 1; Length 661;
Matches 125; Conservative 65; Mismatches 215; Indels 140; Gaps 694 IKRCAGVAGSL------SLVLSTCKNIYSLIVEAS 722 223 VFOSLNEGGTPNLSVIENGLONSTTOSLWLGTEEDIDDEDISSAMLKGLCENSVE3LNLO 282 643 YIPS-----RAVSLEPNWKQEFRTLEVTLRDFSKLNKQDIT---YLGKIESSATSLRLQ 693 167 ----PKDFPÅRNLKVLDFONNÅIHYISREDMRŠLEOAINLSLNFNGNNVKGIEL:AFDST 222 599 FEHLPNCASALDFIKLDEYGGA------MASWEKA------AEDTGGIHMSEAPET 642 127 ----LK------HLFLIQTGISNL--EFIPVHNLENLESLYLGSNHISSIKF-- 166 542 EQEILKAININSEVECGIHLYOBSTSKSALSQEE---EAFFQGKSLYINSGNI;DYLFDE 598 486 TYSSLLRYTCGSSVEATRAVMK--HLAAVYQHGCLLGLSIAKRPL--WRQESIQSVKNTT 541 72 TESRLMNLT---FLDLTRCQINWIHEDTFQSHHQLSTLVLTGNPLIFMAETSLNGPKS-- 126 24;

542 EOETLKAININSFVECGIHLYOESTSKSALSOEF---EAFFOGKSLYINSGNIPDYLFDF 598

Qy Ma Qy Db	G	
Query Match Best Local Similarity 2.7%; Score 142; DB 2; Length 661; Matches 125; Conservative 65; Pred. No. 0.0035; Length 661; 486 TYSSLLRYTCGSSVEATRAVMKHLAAVYOHGCILGLSIAKRPLWROESLQSVKNTT 5.1 72 TFSRLMNLTFLDLTRCQINWIHEDDTECCH	Sequence 4 Application US/08833823  Patent No. 559093  GENERAL INFORMATION: APPLICAMN: JGCODS, Kenneth APPLICAMN: Kelleber, Ken TITLE OF INVERTION: MCKEOUGH TITLE OF INVERTION: MCKEOUGH TITLE OF INVERTION: MCKEOUGH TITLE OF INVERTION: MCKEOUGH CORRESSEE: 87 Cambridge INCO-DD THEREBY TATE CONTROL USA ADDRESSEE: 87 Cambridge Inc Legal Affairs COMPUTER: 187 Cambridge Inc Legal Affairs COMPUTER READABLE FORM: COMPUTER: COMPUTER READABLE FORM: COMPUTER: COMPUTER READABLE FORM: C	Db 390

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US-08-519-547A-6
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                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WordPorfect 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                 NAME: HALEY, JAMES F.
REGISTACHON NUMBER: 27,794
REFERENCE/DOCKET NUMBER: VO
TELECOMMUNICATION INFORMATION:
                                                                                                                                       FILING DATE: 26-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                            FILING DATE: 25 CLASSIFICATION:
                                    TELEFAX:
                                                                                                                                                         APPLICATION NUMBER: EP94113378.7 FILING DATE: 26-AUG-1994
                                                   TELEPHONE:
                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Vertebrate MHC Class II Genes, DNA Sequences
and Pharmaceutical Compositions
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MOLECULE TYPE: DNI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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STRANDEDNESS: do
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                                                                                                                                   ATTPQLKSLETLNLSQNNITDLGAYKLAEALPSL------
                                                                                                                                                                                                                                             GSLSLVLSTCKNIYSLMVEASPLTIED-ERHITSVTNLKTLSIHDLQNQRL----PGGLT 756
                                                                                                                                                                                                                                                                                                              IPSRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAG--VA 701
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                                VLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKL
                                                                 -- AASLLRISIYNNCICDVGAESLARVLPDMVSLRVMDVQYNKFTAAGAQQLAASLRRCP 1100
                                                                                                                                                                                                          GELPAVRDLKKLEFALGPVSGPQAFPKLVRILTAFSSLQHLDLDALSENKIGDEGVSQLS
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                                                                                                    SEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSENYLEKDGNEALHELIDRMN
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Search completed: March 25, 2002, 10:55:40 Job time: 40 sec

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10.6 123 17 AAR98217 Neuron 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM17392 Peptid 7.0 73 22 AAM19302 Peptid 7.0 73 22 AAM193141 Human 7.0 Peptid 5.6 953 20 AAM1145 Peptid 7.0 Peptid 5.6 953 22 AAB20084 Peptid 7.0 Peptid 7	Human (	AAB20081	22	490		179.5	
10.6 1232 17 AAR98217 Neuron 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM15552 Peptid 7.0 73 22 AAM15552 Peptid 7.0 73 22 AAM15552 Peptid 5.6 953 20 AAY11141 Apopto 5.2 953 22 AAB20080 Murine 5.2 953 22 AAB20080 Murine 5.2 953 22 AAB20080 Murine 6.2 953 22 AAB20675 Mouse 6.2 779 22 AAB20510 Human 4.0 1473 22 AAB26758 Human 4.0 1473 22 AAY72673 Human 4.0 1473 22 AAY72670 Human 6.0 1473 22 AAY72670 Human 6.0 1473 22 AAY72670 Human 6.0 1473 22 AAY72671 Human 6	Human (	AAY31142	20	490		179.5	
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10.6 1232 17 AAR98217 Neuron 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM17392 Peptid 7.0 73 22 AAM173141 Human 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0 7.0	Porphoi	AAY34568	20	1266	3.4	180.5	
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10.6 1232 17 AAR98217 Neuron 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM5439 Peptid 7.0 73 22 AAM5439 Peptid 7.0 73 22 AAM5439 Peptid 7.0 73 22 AAM55439 Peptid 5.6 953 21 AAB15552 Apopto 5.6 953 22 AAB20080 Human 5.2 953 20 AAY31145 Murine 7.0 953 22 AAB20084 Murine 7.0 1429 22 AAB25610 Human 4.0 1429 22 AAB25610 Human 4.0 1473 22 AAY72673 Human 4.0 1473 22 AAY72679 Human 9.0 1473 22 AAY72670 Human 9.0 1473 22 AAY72671 Human 9.0 1474 22 AAY72674 Human 9.0 1474 42 42 42 AAY72674 Human 9.0 14	Arabido	AAG48480	21	1374	٠	183	
10.6 123 17 AAR88217  Neuron 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM55439 Peptid 7.0 73 22 AAM55439 Peptid 5.6 953 20 AAR351552 Apopto 5.6 953 22 AAB20080 Human 7.5 2 953 20 AAR31145 Pertid 7.0 953 22 AAB20080 Pertid 7.0 953 22 AAB20080 Pertid 7.0 953 22 AAB20080 Pertid 7.0 953 22 AAR31145 Pe		AAY72671	22	1442	٠	207.5	
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10.6 1232 17 AARR9217 Neuron 73 22 AAM17792 Peptid 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM15330 Peptid 7.0 73 22 AAM15439 Peptid 7.0 73 22 AAM15439 Peptid 7.0 73 22 AAM15439 Peptid 5.6 953 20 AAY21141 Apopto 5.6 953 21 AAB15552 AAB20080 Murine 5.2 953 22 AAB20084 Murine 5.2 953 22 AAB20084 Mouse 5.2 953 22 AAB20084 Mouse 6.2 953 22 AAB20675 Mouse 6.2 953 22 AAB20675 Muman 6.0 1473 22 AAV727673 Human 6.0 1473 22 AAV727619	-	AAY72670	22	1397		207.5	
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10.6 1232 17 AAR98217 Neuron 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM35439 Peptid 7.0 73 22 AAM55439 Peptid 7.0 73 22 AAM55439 Peptid 7.0 73 22 AAR95141 Human 5.6 953 21 AAR815552 APR20080 Human 5.2 953 22 AAR820080 Human 5.2 953 22 AAR820084 Human 7.2 953 22 AAR820084 Murine 7.2 953 22 AAR82571 Human 7.0 1454 22 AAR95673 Human 7.0 1454 22 AAR95673 Human 7.0 1454 22 AAR95673		AAE06758	22	1473	٠	212	
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10.6 1232 17 AAR98217 Neuron 7.0 73 22 AAM17792 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM30302 Peptid 7.0 73 22 AAM30343 Peptid 5.6 953 20 AAM231141 Human 5.6 953 21 AAB15552 Apopto 5.6 953 22 AAB20080 Human 5.6 953 22 AAB20080 Human 6.2 953 22 AAB20080 Human 6.2 953 22 AAB20084 Mouse 6.2 953 22 AAB20684 Mouse 6.2 779 22 AAB25610 Human		AAB62571	22	1429	4.0	212	
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10.6 1232 17 AAR98217 7.0 73 22 AAM17792 7.0 73 22 AAM30302 7.0 73 22 AAM05439 5.6 953 20 AAY31141	Apoptos	AAB15552	21	953		296	
10.6 1232 17 AAR99217 7.0 73 22 AAM17792 7.0 73 22 AAM30302 7.0 73 22 AAM30302	Human C	AAY31141	20	953		296	
10.6 1232 17 AAR98217 7.0 73 22 AAM17792 7.0 73 22 AAM30302	Peptide	AAM05439	22	73		372	
10.6 1232 17 AAR98217 7.0 73 22 AAM17792	Peptide	AAM30302	22	73	7.0	372	
10.6 1232 17 AAR98217	Peptide		22	73	7.0	372	
	Neurona	S	17	w	10.6	561.5	

## ALIGNMENTS

RESULT AAU02880

AAU02880 standard; Protein; 1024 AΑ

AAU02880;

12-SEP-2001 (first entry)

Human caspase recruitment domain 12 (CARD-12) polypeptide #1.

Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway; cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia; myocardial infarction; inflammatory disorder; crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leprosy; tuberculosis; ischaemic brain injury; hypoxic brain injury; kidney ischaemic propertiesion injury; acute bacterial meningitis; exciteboxic brain damage; liver disease.

Homo sapiens.

WO200130971-A2

03-MAY-2001.

26-OCT-2000; 2000WO-US29643

27-OCT-1999; 99US-0161822.

(MILL-) MILLENNIUM PHARM INC

Bertin J, Robison KE;

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Best Local Similarity
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                      sditstyssllrytcgssveatravmkhlaavyqhgcllglsiakrplwrqeslqsvknt
                                       SDITSTYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWRQESLQSVKNT
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)B; AAS03945.
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2001-308628/32 DB; AAS03946.

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                                                                                                                                                                                                                                    cancer; viral infection; poxvirus; adenovirus; autoimmune disorder;
systemic lupus erythematosis; arthritis; neurological disorder; stroke;
Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease;
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                          Bertin J,
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Matches 1014;
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ated caspase recruitment domain-12 polypeptide and nucleic acids ding them, useful for treating and diagnosing disorders associate abnormal apoptosis such as cancer, arthritis and Alzheimer's ase.
                                            EPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLS
                                                                                                                                        ITCAIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKHKGVAASDFIRSLDHCGDLALEGVF
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98.1%;
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Pred. No. 0;
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17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
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Cao 1
Claim 20;
           Isolated polypeptide for treatment of diseases, antibodies and research use -
                              WPI; 20
N-PSDB;
                                                                                                                                                            tomato; monkey; dog; sea urchin; expressed sequence tag; ES diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                            25-JAN-2001;
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Drmanac 1
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Page 832-833; 1275pp;
                                                                              2000US-0491404.
2000US-0617746.
2000US-0631451.
2000US-0663870.
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                                          eevpqlvklglknwrltdteirilgaffgknplknfqqlnlagnrvssdgwlafmgvfen
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virus

cytostatic;

eczema; anaemia;

23-DEC-1999; 21-JAN-2000; N-PSDB; Isolated human polynuch treatment and diagnosis (HYSE-) 22-DEC-2000; ΥŢ 2001-457603/49 AAH99581 HYSEQ Liu C, ; 99US-0471275. ; 2000US-0488725. ; 2000US-0552317. 2000WO-US35017 polynucleotides encoding diagnosis of e.g. cancer, Drmanac ulcers and HIV

useful for V infection

the

cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoletic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in such as antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiare nervous system; virucide; anti-HIV; fungicide; antimutagen; Claim 20; Page 240; 1217pp; English.

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                                               Neuronal therapy;
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                   Homo sapiens
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38; Conservative
                                              apoptosis inhibitor cancer; AIDS; amyotr
                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human neuronal apoptosis inhibitor protein (AAW20032), or N is a negative regulator of apoptosis, partic neuronal apoptosis and, when deficient or absent, contributes to neurodegenerative phenotypes such as spinal muscular atrophy (SMA) and amyotrophic lateral sclerosis. Its amino acid sequence was deduced from a CDNA clone (AAT71265) obtd. from a human foetal spinal cord cDNA library. NAIP polypeptides, esp. those containing at least two BIR (baculovirus IAP repeat) domains, can be expressed in host-vector systems and used to increase or induce apoptosis for the treatment of AIDS, neurodegenerative disease, myelodysplastic syndromes or ischaemic hnjury, to screen for (ant)agonists, or to produce antibodies useful for inhibiting apoptosis.
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                  EATRA---VMKHLAAVYQHGCLLGLSIAKRPLWRQESLQSVKN--
                                                                                                                      ASDFIR-SLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTAQRFKFKY
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                                                   rflspafqeflagmrlielldsdrqehqdlglyhlkqinspmmtvsaynnflnyv--ssl
                                                                         KFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSV
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                                                                                                                                                                                                                                                                                                                                                                     RAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEF--KPQNCPEIEAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLKSLKEWNYPLFQDLNGQ----SLFHQTSEGDLDD------
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Pred. No. 9.1e-46;
7; Mismatches 410
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N-PSDB; AAX58000.
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                                                                       (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
(SAKA/) SAKAI H.
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Best Local Similarity
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                                                      1007
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                                                                                                                                                                                                                                                                                                 LKAI----NINSFVECGIHL------YQESTSKSALSQEFEAFFQGKSLYINSGNIPD 593
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                  IEDERHITSVTNLKTLSIH----DLQNQRLPGGLTDSLGNLKNLTKLIMDNIKM-----
                                                   ndidvvgqdmleilmtvfsasqrielhlnhsrgfiesirpalelskasvtkcsisklels
                                                                                     RDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCK-NIYSLMVEASPLT
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                                                                                                                                                              The present sequence represents a human apoptosis inhibitory protein The apoptosis inhibitory protein is useful for the elucidation of the mechanism of various apoptosis diseases such as human spinal muscular atrophy and the diagnosis, the prevention and the treatment
                                                                                                                                                                                                                                                            New apoptosis inhibitory protein - useful for determining mechanism of various apoptotic diseases e.g. human spinal muscular atrophy
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                                                                                                                           Sequence
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spinal muscular atrophy.
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                            FLKSLKEWNYPLFQDLNGQ----SLFHQTSEGDLDD-----
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                                                       12.4%; Score 653; DB 20; 23.7%; Pred. No. 9.1e-46; tive 197; Mismatches 410
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                                                                                                                   Matches
                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                      by hybridomas, prepared by fusing antibody-producing cells of mammals immunized with an immunogen containing residues 256-586 or 841-1052 of a 1403 residue amino acid sequence, fully defined in the specification, or their partial sequence, with a myeloma cell line. The monoclonal antibodies are for the study of apoptosis disease onset mechanism, disease diagnosis and development of drugs to prevent and treat apoptosis-related diseases. The quantitation method with the monoclonal antibodies is simple and accurate by using a biological specimen. This sequence represents the human apoptosis inhibitory protein NAIP which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                          Simple and accurate quantitation of human apoptosis inhibitory protein (NAIP) with monoclonal antibodies, for disease diagnosis and development of drugs to prevent and treat apoptosis-related diseases
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Region
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                This invention describes novel anti-NAIP monoclonal antibodies, produced
                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 24-30; 36pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakai H,
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apoptosis disease onset mechanism; drugs development; prevention;
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(SAKA/) SAKAI H.
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                                                                                                                 Score 653; DB 21;
Pred. No. 9.1e-46;
7; Mismatches 410
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sqcvlrlprlirlnmlswlldaddiall 1374
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                                                                                                       GKNPLKNEQQLNLAGN-RVSSDGWLAFMGVFENLKQLVFFDFS---TKEFLPDPALVRKL 987
                                                                                                                                            nlee---lilptgdgiyrvakliiqqcqqlhclrvlsffktlnddsvveiakvaisggf- 129:
                                                                                                                                                                               VLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRLTDT-----EIRILGAFF 931
                                                                                                                                                                                                                -ckklteikfsdsff--qavpfva-slpnfislkilnleggqfpdeetsekfayilgsls 1235
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                                                                      -----qklenlklsinhkiteegyrnffgaldnmpnlgeldisrhftecikaqattvksl 1346
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Matches 261
                                                                                                                                                                                                                                                                                                                                Novel human neuronal apoptosis inhibitor protein (AAW20033), or NJ is a negative regulator of apoptosis, partic neuronal apoptosis and, when deficient or absent, contributes to neurodegenerative phenotypes such as spinal muscular atrophy (SNA) and amyotrophic lateral sclerosis. Its amino acid sequence was deduced from a CDNA clone (AAT71266) obtd. from a human foetal spinal cord cDNA library. NAIP polypeptides, esp. those containing at least two BIR (baculovirus IAP repeat) domains, can be expressed in host-vector systems and used to increase or induce apoptosis for the treatment of AIDS, neurodegenerative disease, myelodysplastic syndromes or ischaemic injury, to screen for (ant)sgonists, or to produce antibodies useful for inhibiting apoptosis.
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Misc-difference 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 41; Fig 7A-L; 102pp; English
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New neuronal inhibitor of apoptosis - useful for diagnosing treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
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rpdeglasilcdqllekegsvtemcmrnilqqlknqvlfllddykeicsipq---vigkl 566
                                                                                                                                                LAQDLKDLYHTPSFLNF-------
                              RAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEF - - KPQNCPEIEAL
                                                         \tt qeplvlpevfgnlnsvmcvegeagsgktvllkkiaflwasgccpllnrfqlvfylslsst
                                                                        VEQLTLNGLLQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLS---
                                                                                                                                                                                                        FLKSLKEWNYPLFQDLNGQ----SLFHQTSEGDLDD-----
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23.7%; Pro
ative 196;
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                                                                                                                                                                                                                                  Score 652; DB 18;
Pred. No. 1.1e-45;
06; Mismatches 418;
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Gonadotropic hormone; excessive ovulation animal; transgenic animal;

Gonadotropic

hormone protein sequence

20-JUL-1999

(first entry)

AAY14080

AAY14080 standard; Protein;

1295

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The invention relates to an excessive ovulation animal, which is a transgenic animal with a totipotent cell containing a DNA fragment containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The excessive ovulation animal is useful for improving the productivity of animals.
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(SAKA/) SAKAI H.
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                              EATRA---VMKHLAAVYQHGCLLGLSIAKRPLWRQESLQSVKN-----
                                                      rflspafqeflagmrlielldsdrqehqdlglyhlkqinspmmtvsaynnflnyv--ssl
                                                                                   KFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSV
                                                                                                                                ASDFIR-SLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTAQRFKFKY
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RESULT 11
AAY09540
                    The present sequence represents a human apoptosis inhibitory protein. The apoptosis inhibitory protein is useful for the elucidation of the mechanism of various apoptosis diseases such as human spinal muscular atrophy and the diagnosis, the prevention and the treatment
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          of such
                                                                                Claim
                                                                                                       New apoptosis inhibitory protein - of various apoptotic diseases e.g.
                                                                                                                                             N-PSDB;
                                                                                                                                                          WPI; 1999-323531/27
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                                                                                                                                                                                                                                                                                                                                                                   Human apoptosis
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          diseases
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                                                                                                        useful for determining mechanism human spinal muscular atrophy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 FLKSLKEWNYPLFQDLNGQ----SLFHQTSEGDLDD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLFD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAQDLKDLYHTPSFLNF------YPLGEDIDIIFNLKSTFTEPVLWRKDQHHHR
                                                                                                                                                                                                                                                                                                                                                rnlaekednvksymdmgrraspdlstgywklspkgykip--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKAI----NINSFYECGIHL-----YQESTSKSALSQEFEAFFQGKSLYINSGNIPD 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pstkagpkivshllhlvdn------keslenisenddylkhqpeislqmql 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEQLTLNGLLQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLS--
                                                                                                                                                                                            aaeqellltlpsleslevsgtiqsqdqifpn--ldkflclkelsvdlegninvfsvipee 1124
                                                                                                                                                                                                                                                                                                                                                                                                                          yffdhpeslsllrsihfpirgnktsprahfsvletcfdksqvptidqdyasafepmnewe 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EATRA---VMKHLAAVYQHGCLLGLSIAKRPLWRQESLQSVKN------TTEQEI 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KFFHKSFQEYTAGRRLSSLLTSHEDEEVTKGNGYLQKMVSISDITSTYSSLLRYTGGSSV 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vyfgknqslqkiqktplfvaaicahwfqypfdpsfddvavfksymerlslrnk----a
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                                                                                                                                                                                                                                  IEDERHITSVTNLKTLSIH----DLQNQRLPGGLTDSLGNLKNLTKLIMDNIKM------
                                                                                                                                                                                                                                                                      ndidvvgqdmleilmtvfsasqrielhlnhsrgfiesirpalelskasvtkcsisklels 1066
                                                                                                                                                                                                                                                                                                            RDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCK-NIYSLMVEASPLT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lrglwqicpqayfsmvsehllvlalktayqsnt-vaacspfvlqflqgrtltlgalnl-q 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASDFIR-SLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTAQRFKPKY 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKHKGVA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iqknhlsrtclliavrtnrardirryletileikafpfyntvcilrklfshnmtrlrkfm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpdeglasicdqllekegsvtemcmrniiqqlknqvlfllddykeicsipq---vigkl
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                                    -ckklteikfsdsff--qavpfva-slpnfislkilnlegqqfpdeetsekfayilgsls 1235
                                                                          PC-DLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDL-SENYLEKDGNEALHELIDRMN 876
                                                                                                                fpnfhhmeklliqisaeydpsklvkliqnspnlhvfhlkcnffsdfgslmtmlvs----
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                                                                                                                                                      -----NEEDAIKLAEGLKNLKKMCLFHL--THLSDIGEGMDYIVKSLSSE 818
                                                                                                                                                                                                                                                                                                                                                                                    -----KAAEDTGGIHMEEAPETY-IPSRAVSLFFNWKQEFRTLEVTL 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.28;
24.48;
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Pred. No. 1.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                --FFEHLPNC--ASALDFIKLDFYGG--AMASWE 625
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В QΥ

69

FLKSLKEWNYPLFQDLNGQ----SLFHQTSEGDLDD-----

Conservative

155;

Mismatches

341;

Indels

215;

Gaps

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100

344 flqnmks-saevtpdlqsrgelcellettsesnledsiavgpivpemaggeaqwfqeakn 402

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RESULT 12
AAR98217
                                                                                            В
                                                                                                                                      This sequence represents the human neuronal apoptosis inhibitor protein (CC (MAIP). The cDNA encoding this sequence was found on a region of the CDNA encoding this sequence was found on a region of the CC artificial chromosome 5q13. This sequence was isolated from a yeast CC artificial chromosome (YAC) contig containing the D58435-D58112 interval CC of the chromosome 5q13. Mutations in the NAIP gene, are causative of CC spinal muscular atrophy (SMA) types I, II, and III. SMAs are a group of CC autosomal recessive, neurodegenerative disorders. SMAs are classified CC into the three types based upon the age of onset (with type I being the CC severest form with the earliest age of onset). All three types are CC severest form with the degeneration of the alpha motor neurons of the CC spinal cord manifesting as weakness and wasting of the proximal voluntary CC muscles. The most common mutations of the NAIP gene sequence are thought to be deletions of exons 5 and 6, and reductions in the copy number of CC used for the diagnosis of SMA, and for directing the formulation of CC used for the diagnosis of SMA, and for directing the formulation of CC conventional and genetic therapies for SMA. Identification of genes showing homology with the NAIP locus, and proteins that interact with
Query Match
Best Local Similarity
Matches 226; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHKJ )
(UYOT-)
                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 68-70; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuronal apoptosis inhibitor protein for use in the diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-222003/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spinal cord;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTTAWA.
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94GB-0021019
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                    10.6%; Score 561.5; DB 1 24.1%; Pred. No. 4.1e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene - used to develop prods. of spinal muscular atrophy
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                                    DB 17;
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 Probe;
                                                                12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                           1067
                                Peptide #4226
                                                                                                                                                                                                            1185 ----nleelilptgdgiyrvakliiqqcqqlhclrvl 1217
                                                                                                                                                                                                                                                                                                                                                                                                             1007
                                                                                                                              AAM17792 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rflspafqeflagmrlielldsdrqehqdlglyhlkqinspmmtvsaynnflnyv--ssl
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                                                                                                                                                                                                                                                                                                                                                                         IEDERHITSVTNLKTLSIH----DLQNQRLPGGLTDSLGNLKNLTKLIMDNIKM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lrglwqicpqayfsmvsehllvlalktayqsnt-vaacspfvlqflqgrtltlgalnl-q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKAI----NINSFVECGIHL------YQESTSKSALSQEFEAFFQGKSLYINSGNIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pstkagpkivshllhlvdn-------keslenisenddylkhqpeislqmql 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASDFIR-SLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTAQRFKPKY 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKHKGVA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAQDLKDLYHTPSFLNF-----YPLGEDIDIIFNLKSTFTEPVLWRKDQHHHR 148
                                                                                                                                                                                                                                              SEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSIL 853
                                                                                                                                                                                                                                                                                                           -----SDIGEGMDYIVKSLS 816
                                                                                                                                                                                                                                                                                                                                                                                                         ndidvvgqdmleilmtvfsasqrielhlnhsrgfiesirpalelskasvtkcsisklels
                                                                                                                                                                                                                                                                                                                                                                                                                                          RDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCK-NIYSLMVEASPLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rnlaekednvksymdmqrraspdlstgywklspkqykip-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yffdhpeslsllrsihfsirgnktsprahfsvletcfdksqvptidqdyasafepmnewe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EATRA----VMKHLAAVYQHGCLLGLSTAKRPLWRQESLQSVKN------TTEQEI 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSV 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iqknhlsrtclliavrtnrardirryletileiqafpfyntvcilrklfshnmtrlrkfm 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKELA--EGLL 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpdeglasiicdqllekegsvtemcmrniiqqlknqvlfllddykeicsipq---vigkl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \tt qeplvlpevfgnlnsvmcvegeagsgktvllkkiaflwasgccpllnrfqlvfylslsst
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lneqlraaytsasfrhmslldissdlatdhllgcdlsi---askhiskpv------
human; microarray;
                                                              (first entry)
                           encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KAAEDTGGIHMEEAPETY-IPSRAVSLFFNWKQEFRTLEVTL 666
gene
                                                                                                                                73
expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FFEHLPNC--ASALDFIKLDFYGG--AMASWE
 cervical
epithelial
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В
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                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to human single exon nucleic acid probes (SEN: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                         1004 GWQFDDDDLSVIT 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
26-MAY-2000;
                                                                                                                                                      AAM30302 standard; Protein; 73
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer
                     Homo sapiens
                                            genetic
                                                       Probe; microarray;
                                                                               Peptide #4339 encoded
                                                                                                      17-OCT-2001
                                                                                                                              AAM30302;
                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                               cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001;
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                                                                                                                                                                                                                                                            944 LAGNRVSSDGWLAFMGVFENLKOLVFFDFSTKEFLPDPALVRKLSQVLSKLTFLQEARLV 1003
                                                                                                                                                                                                               61
                                                                                                                                                                                                              gwqfddddlsvit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                        Similarity
                                            disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 22618; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                       73
                                                                                                                                                                                                                                                                                                          7.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0234687.
2000US-0236359.
2000GB-0024263.
                                                                                                      (first entry)
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2000US-0207456
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2000US-0632366
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                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                               73
                                                         human;
                                                                              γd
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                                                                               probe
                                                       placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Σ
                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                     Score 372; DB 22;
Pred. No. 5.2e-24;
                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
                                                                                for
                                                                                                                                                                                                                                                                                                           Mismatches
                                                                             measuring placental gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
                                                         antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                         ot form part of the printed format directly from WIPO
                                                                                                                                                                                                                                                                                                                                  Length 73;
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AC XX 
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AAM05439
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Best Local Similarity
Thehes 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1004 GWQFDDDDLSVIT 1016
                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                   WO200157270-A2
                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #4121 encoded by probe for measuring breast gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM05439 standard; Protein; 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human placenta.
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                                                                                                                                                                29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID No 30571; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                            inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
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27-SEP-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 944 LAGNRVSSDGWLAFMGVFENLKQLVFFDFSTKEFLPDPALVRKLSQVLSKLTFLQEARLV 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l lagnrvssdgwlafmgvfenlkglvffdfstkeflpdpalvrklsgvlskltflgearlv 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gwqfddddlsvit 73
                                                                                                                                                                                                                                                                                                                                                                                                          human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression in human placenta
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2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.0%; Score 372; DB 22; ilarity 100.0%; Pred. No. 5.2e-24; Conservative 0; Mismatches 0;
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456.
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                                                                                                                                                                                                                                                                                                                                                                                                          breast disease; breast cancer;
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                                                                                                                                                                                                                          Note: The sequence data for this patent did not specification, but was obtained in electronic for at ftp.wipo.int/pub/published_pct_sequences.
                                1004 GWQFDDDDLSVIT 1016
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                                                                                 LVPTGDGIHQVAKLIVRQCLQLPCLRVLAFHD-ILDDESVIEIGEAATSGSFQKLENLDI
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                                                                                                                                                                                      LVSCCLSA-NAVKILAQNLHNLVKLSILDL-SENYLEKDGNEALHELIDRMNVLEQLTAL 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01282; BIR_REPEAT_1; 2.
PROSITE; PS50143; BIR_REPEAT_2; 3.
Apoptosis; Repeat; Multigene family.
REPEAT 60 127 BIR 1.
REPEAT 159 227 BIR 2.
REPEAT 278 345 BIR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1858256; Birc1g.
InterPro; IPR001370; BIR.
Pfam; PF00653; BIR; 3.
SMART; SM00238; BIR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20414747; PubMed=10958627;
Endrizzi M.G., Hadinoto V., Growney J.D., Miller W.,
"Genomic sequence analysis of the mouse Naip gene arz
Genome Res. 10:1095-1102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNALS.
-!- SIMILARITY; CONTAINS 3 BIR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF242433; AAF82749.1; -.
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                                                                                                                                                                                                                                                                                                                                                                       149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                           VEQUILINGLIQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLS--
                                                                                                                                                                                                              RAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFK--PQNCPEIEAL
                                                                                                                                                                                                                                                                                                        QGALTIPEVESNLSSVMCVEGEAGSGKTTFLKRIAFLWASGCCPLLYRFQLVFYLSLSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                 LSEQLEDTYTKTSFCHMNLPEVCSSLGTDHLLSCDVSII---SKHISQPV------
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LQIQKSRCLRNLMKTPLFVVITC-AIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKHKGV
                                                            ITKNYLFRTCLLIAVHTNRVRDIRPYLGTSLEIQEFPFYNTVFVLRKFFSHDIICVEKLI
                                                                                                                                                                                  TPDQGLDNIICTQLLGAGGCISEVCLSSSIQQLQHQVLFLLDDYSGLASLPQ---ALHTL
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                                                                                                                     IKENHREKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKEL--AEGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253;
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278 3
1402 AA;
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24.3%;
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159662 MW; C1DFFBA359893E0D CRC64;
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                                                                                                                                            BIR1_HUMAN STANDARD; PRT; 1403 AA. Q13075; Q137730; Q99796; Q75857; Q1-NOV-1997 (Rel. 35, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
BACULOVIRAL IAP REPEAT-CONTAINING PROTEIN 1 (
                                                                                                   BIRC1 OR NAIP.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                      1354
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                            SEQUENCE FROM
                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
TISSUE=Fetal brain;
MEDLINE=95112344; F
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                                                                                                                                                                                                                                                                                                      SLTRLGMLSWLLDEEDMKVI 1373
                                                                                                                                                                                                                                                                                                                                                                                                                          LVPTGDGIHQVAKLIVRQCLQLPCLRVLAFHDILDDESVIEIGAATSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QALLQVLMEVFSASQSIEFHLFNSSGFLESIRPALELSKASVTKCSMSRLELSRAEQELL 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVRGLWLVSPESFSSFV--SEHLERLALIFAYESNTVAECSPFILQFLRGRTLALRVLNL
                                                                                                                                                                                                                                                                                                                                                                                           L---AGNRVSSDGWLAFMGVFENLKQLVFFDFSTKEFLP-----DPALVRKLSQVLSKLT 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPLKNFQQL-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGQCFEAMTFVNILP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAESLQATVSSCGQLALTGLFSSCFEFNSDDLAEAGVDEDVKLTTFLMSKFTAQRLRPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AASDFIRSLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTAQRFKPKY
                                                                                                                                                                                                                                                                                                                               FLQEARLYGWQFDDDDLSVI
                                                                                                                                                                                                                                                                                                                                                              LDISMNHKITEEGYRNFFQALDNLPNLQMLNICRN--IPGRIQVQATTVKALCHCVSRLP 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSIRT--STESDLSKLVKFIQNFPNLHVFHLK--CDFLSNCESLMTALAS--CKKLREIE
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                            N.A.
PubMed=7813013;
                                                                  Chordata; Primates;
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                                                                      Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                        Hominidae;
                                                                                                                                                (NEURONAL APOPTOSIS
                                                                                    Euteleostomi;
                                                                        HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                       SFOKLEN
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"Suppression of apoptosis in mammalian cells by i family of IAP genes.";
Nature 379:349-353(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MacKenzie A.E.;
"Sequence of a 131-kb regionatrophy candidate genes SM Genomics 48:121-127(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy N., Mahadevan M.S., McLean M., Shutler G., Yaraghi Z., Farahini R., Baird S., Besner Johnston A., Lefebvre C., Kang X., Salih M., Aubry H., Tamai K., Guan X., Ioannou P., Crawford T.O., de Jong P.J., Surh L., Ikeda J., Korneluk R.G., Mackenzie A.; "The gene for neuronal apoptosis inhibitory protein is partially deleted in individuals with spinal muscular atrophy."; Cell 80:167-178(1995).
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Jones K., Graves T., McPherson J.;

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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Xuan J.-Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Liver;
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         SPINAL CORD.

SPINAL CORD.

DISEASE: MUTATED OR DELETED FORMS OF NAIP HAVE BEEN FOUND IN

INDIVIDUALS WITH SPINAL MUSCULAR ATROPHY TYPE I (SMA TYPE I). SMAS

ARE FATAL AUTOSOMAL RECESSIVE DISORDERS SUBCLASSIFIED AS TYPE I

(WERDNIG-HOFFMANN DISEASE), TYPE II (INTERNEDIATE FORM), AND TYPE

III (WOHLFART-KUGELBERG-WELANDER DISEASE) BASED UPON THE AGE OF

ONSET AND CLINICAL SEVERITY. THESE NEURODEGENERATIVE DISORDERS ARE

CHARACTERIZED BY DEGENERATION OF LOWER MOTOR NEURONS, LEADING TO

PROGRESSIVE PARALYSIS MUSCULAR ATROPHY. CONCERNS 1 IN 6000
                                                                                                                                                                                                                                                  SIGNALS.
TISSUE SPECIFICITY: EXPRESSED IN MOTOR
TO LIVER AND PLACENTA,
                                                                                                                                                                                                                                                                                                                                 FUNCTION: PREVENTS
SIMILARITY: CONTAINS 3 BIR REPEATS.
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Y., Kang X., Lefebvre
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Lefebvre C., Ikeda
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between the Swiss Institute of pioinformatics and the it the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar Apoptosis; REPEAT EMBL; U19251; AAC52045.1; EMBL; U80017; AAC52047.1; EMBL; U21913; AAA64504.1; PROSITE; PS01282; BIR\_REPEAT PROSITE; PS50143; BIR\_REPEAT InterPro; IPR001370; BI
Pfam; PF00653; BIR; 3.
SMART; SM00238; BIR; 3. EMBL; AC005031; AAC62261.1; entities requires a MIM; 600355; SWISS-PROT entry is copyright. It is produced through a collaboration s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch). Repeat. BIR\_REPEAT\_1; BIR\_REPEAT\_2; BIR. BIR 21 restrictions and for in no way

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FPNFHHMEKLLIQISAEYDPSKLVKLIQNSPNLHVFHLKCNFFSDFGSLMTMLVS--
                                                                                                                                             RDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCK-NIYSLMVEASPLT
                                                                                                                                                                            RNLAEKEDNVKSYMDMQRRASPDLSTGYWKLSPKQYKIP-----
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                                                       AAEQELLLTLPSLESLEVSGTIQSQDQIFPN--LDKFLCLKELSVDLEGNINVFSVIPEE
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PK -> YR (IN REF. 3).

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MW: 566304C154DA5E64 C
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Pred. No. 6.
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BIRCLE OR NAIP5 OR NAIP-RS3.
EMBL; AF135492; AAD56764.1; -. EMBL; AF131205; AAD56760.1; -. EMBL; U66326; AAC52974.1; -. MGD; MGI:1298220; Bircle.
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Genomics 38:405-417(1996).
Genomics 38:405-417(1996).
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Endrizzi M., Huang S., Scharf J.M., k
Kunkel L.M., Miller W., Dietrich W.F.
"Comparative sequence analysis of the
interval.";
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Huang S., Scharf J.M., Growney J.D., Endriz
"The mouse Naip gene cluster on Chromosome
functional transcripts.";
Mamm. Genome 10:1032-1035(1999).
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scharf J.M., Damron D., Frisella A., Bruno S., Beggs A.H., Kunkel L.M., Dietrich W.F.; "The mouse region systemic for human spinal muscular atrophy lies within the Lgnl critical interval and contains multiple copies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1292
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                                                                                                                                        email to license@isb-sib.ch).
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EHISEWRRNFAQDEEIIKNYENIRPRALPDISEGYWKLSPKPCKIPKLEVQVNNTDAADQ
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Q9QUK4; Q9R030; CO99124;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
BACULOURAL LAP REPEAT-CONTAINING PROTEIN 1B (NI
INHIBITORY PROTEIN 2).
BIRC1B OR NAIP2 OR NAIP-RS6.
Mus musculus (Mouse).
Mus musculus (Mouse)
Mammalia: Eutheria; Rodentia; Sciurognathi; Muri
                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE-99315342; PubMed-10384056;

Yaraghi Z., Diez E., Gros P., MacKenzie A.;

"cDNA cloning and the 5'genomic organization
gene for murine Legionella resistance.";

Mamm. Genome 10:761-763(1999).
                                                                                                          STRAIN=129/SV;
MEDLINE=99417674; PubMed=10486205;
Endrizzi M., Huang S., Scharf J.M.,
Kunkel L.M., Miller W., Dietrich W.,
"Comparative sequence analysis of ti
                                                                                                                                                                                                                                                                                                                             MEDLINE=99431676; PubMed=10501978; Huang S., Scharf J.M., Growney J.D., Endrize The mouse Naip gene cluster on Chromosome functional transcripts.";
            STRAIN=129/SVJ;
MEDLINE=97131520; PubMed-8975718;
Scharf J.M., Damron D., Frisella
Kunkel L.M., Dietrich W.F.;
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Best Local Similarity 24.2
Matches 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U66329; AAC52977.1; ...
MGD; MGI:1198226; BirCib.
InterPro; IPR001370; BIR
Pfam; PF00053; BIR; 3.
SMART; SM00238; BIR; R.
PROSITE; PS01282; BIR, REPEAT_1; 2.
PROSITE; PS50143; BIR_REPEAT_2; 3.
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exon 5
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Genomics 38:405-417(1996).
Genomics 38:405-417(1996).
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EMBL; AF135490; AAD56762.1; -.
EMBL; AF102871; AAC73002.1; -.
EMBL; AF131205; AAD56759.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis;
REPEAT
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                                                                                                                                                                                            445
                                                                                                                                                                                                                                         404 VSVLCRDQ-DHSEAQG------RGCASSGTYLPS-----TDL-GQSEAQWLQEA-
                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                  38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNALS: SIMILARITY: CONTAINS 3 BIR REPEATS
                      LLQIQK-----SRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKN 374
                                                                                                                                             ---QGSLTIPEVFSNLNSVMCVEGEAGSGKTTFLKRIAFLWASGCCPLLNRFQLVFYLSL
                                                                                                                                                                                                          LDDLAQDLKDLYHTPSFLNF------YPLGEDIDIIFNLKSTFTEPVLWRKDQH 145
IMRVRKFINYFGFHEELQGIHKTPLFVAAVCTDWFKNPSDQPFQDVALFKAYMQYL----
                                               HTLITKNYLSRTCLLIAVHTNKVRGIRPYLDTSLEIKEFPFYNTVSVLRKLFSHD-----
                                                                      EALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKELAEGL
                                                                                             SSITPGQELAKIICAQLLGAGGCISEVCLSSIIQQLQHQVLFLLDDYSGLASLPQ---AL
                                                                                                          SRAQGG--LFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFK--PQNCPEI
                                                                                                                                                         HHRVEQLTLNGLLQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRL
                                                                                                                                                                                           -RSLSEQLRDTYTKATFRHMNLPEVYSSLGTDHLLSCDVSII---SKHISQPV-----
                                                                                                                                                                                                                                                                VNIICCEKVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGD
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SD -> FN (IN)

K -> N (IN)

K -> C (IN)
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2; 3.
family.
BIR 1.
BIR 2.
BIR 3.
D -> G
L -> F
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Pred. No. 1.1e-28;
5; Mismatches 423
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NI)
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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

PROTEIN 1A (NEURONAL APOPTOSIS

update)

Å

NCBI\_TaxID=10090;

Mus musculus (Mouse).

INHIBITORY PROTEIN 1).
BIRC1A OR NAIP1 OR NAIP.

SEQUENCE FROM N.A.

Yaraghi Z., Korneluk R.G., MacKenzle A.E.;

"Cloning and characterization of the multiple copies
homologue of NAIP (neuronal apoptosis inhibitory prot

protein) of the n).";

murine

BIRA\_MOUSE STANDARD; PRT; 1403 AA 09QWK5; 09R017; 09JIB5; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last

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RESULT 6
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                                                                                                    QVLSKLTFLQEARLVGWQFDDDDLSVI
                                                                                                                                                                      NFQQL-NL---AGNRVSSDGWLAFMGVFENLKQLVFFDFSTKEFLPD-----PALVRKLS
                                                                      QCVSRLPSLTRLGMLSWLLDEEDIKVI
                                                                                                                                      GFQKLENLDLTLNHKITEEGYRNFFQVLDNLPNLKNLDIS--RHIPECIQIQAITVKALG
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                                                                                                                                                                                                         EK----LFVPTGDGIHQVAKLIVRQCLQLPCLRVLVFAETLDDDSVLEIAKGATRG
                                                                                                                                                                                                                                         EQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRIL-GAFFGKNPLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AEDTGGIHMEEAPETYIPSRAVSLFFNWK-----QEFRTLEVTLRD
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001370; BIR. Pfam; PF00653; BIR; 3. SMART; SM00238; BIR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF007769; AAB69223.1;
EMBL; AF135491; AAD56763.1;
EMBL; AF242432; AAF82752.1;
MGD; MGI:1298223; Bircla.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endrizzi M.G., Hadinoto V., Growney J.D., Mil
"Genomic sequence analysis of the mouse Naip
Genome Res. 10:1095-1102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01282; BIR_REPEAT_1; PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Huang S., Scharf J.M., Growney J.D., Endriz "The mouse Naip gene cluster on Chromosome functional transcripts.";
Mamm. Genome 10:1032-1035(1999).
                                                                                                                                                                                                                                                                                                                                                                             REPEAT
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20414747;
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DHLIGCDVSII---SKHISQPV------QGALTIPEVFSNLSSVMCVEGETGSGKT
                                                                                                                                                                                    TSEGDLDD----
                                                    MLLKLRQRVLFLLDGYNEFK--PQNCPEIEALIKENHRFKNMVIVTTTTECLRHIRQFGA
                                                                                            TLLQRIAMLWGSGKCKALTKFKFVFFLRLS--RAQGGLFETLCDQLLDIPGTIRKQTFMA
                                                                                                                                      -YPLGEDIDIIFNLKSTFTEPVLWRKDQHHHRVEQLTLNGLLQALQSPCIIEGESGKGKS
                                                                                                                                                           TSESNHDDPAAVHSTVVGLGRSEAQWFQEARSLSEQLRDNYTKATFRHMNLPEVCSSLGT 430
                                IIQQLQHQVLFLLDDYSGLASLPQ---ALHTLITKNYLSRTCLLIAVHTNRVRGIRSYLD
                                                                         TFLKRIAFLWASGCCPLLYRFQLVFYLSLSSITPDQGLANIICAQLLGAGGCISEVCLSS
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24.7%;
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Pred. No. 1.2e-28;
5; Mismatches 409
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SEQUENCE FROM N.A.
STRAIN-NOD; TISSUE-Spleen;
MEDLINE-97152412; PubMed-8995190;
Sims T.N., Elliott J.F., Ramassar

Ramassar V.,

Denney

D.W. Jr.,

Halloran

Eukaryota; Metazoa; Mammalia; Eutheria; NCBI\_TaxID=10090;

Chordata; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Mus

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C2TA_MOUSE
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                                                                                                                   P79621; Q31115;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MHC CLASS II TRANSACTIVATOR CIITA.
MHC2TA OR CIITA OR C2TA.
Mus musculus (Mouse).
                                                                                                                                                                                                                                C2TA_MOUSE
                                                                                                                                                                                                                                                                                                              1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCASALDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSRAVSLFF------
                                                                                                                                                                                                                                                                                                                                                                                                                                      QFPDKETSEKFAQALGSLRNLEE----LLVPTGDGIHQVAKLIVRQCLQLPCLRVLAFHYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWKQ-----EFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVL
                                                                                                                                                                                                                                                                                                                                         FSTKEFLPD-----PALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVI 1015
                                                                                                                                                                                                                                                                                                                                                                           LDNDSVIEIARVATSGGF-----QKLEKLDLSMNHKITEEGYRNFFQALDNLPNLQ--N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CDFLSNCDSLMAVLAS--CKKLREIEFSGRCFEAMPFVNILP----NFISLKILNLISQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELSKASVTKCSMSRLELSRAEQELLLTLPALQSLEVS--ETNQLPDQLFHNLHKFLGLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQDV--SSVNEDVLLTTGLLCKYTAQRFKPKYKFFHKSFQEYTAGRRLSSLLTSHEPEEV 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENPSDQPFQDMALFKSYMQYL----SLKHKG-AAKPLQATVSSCGQLALTGLFSSCFEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----GNLKNLTKLIMDNIKM---NEEDAIKLAEGLKNLKKMCLFHLTH 800
                                                                                                                                                                                                                                   STANDARD;
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Query Match
Best Local S
Matches 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             poorly responsive to IFNgamma stimulation: increase in tumor immunogenicity is accompanied by induction of a mouse class transactivator and class II MHC.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mouse class II transactivator: cDNA sequence and amino acid comparison with the human class II transactivator."; Immunogenetics 45:220-222(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer Immunol. Immunother. 42:99-107(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Panelli M.C., Wang E., Shen S., Schluter S.F., Hersh E.M., Stopeck A., Gangavalli R., Barber :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/C; TISSUE=Thymus; MEDLINE=96188886; PubMed=8620527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; Activator; ATP-binding.

52 138 ASP/GLU-RICH (ACIDIC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akporiaye E.T.
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  470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: ESSENTIAL FOR TRANSCRIPTIONAL ACTIVITY OF THE HLA CI
II PROMOTER; ACTIVATION IS VIA THE PROXIMAL PROMOTER; NO DNA
BINDING OF IN VITRO TRANSLATED CIITA WAS DETECTED. MAY ACT IN
COACTIVATOR-LIKE FASHION THROUGH PROTEIN-PROTEIN INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTACTING FACTORS BINDING TO THE PROXIMAL MHC CLASS II PROMOTER, TO ELEMENTS OF THE TRANSCRIPTION MACHINERY, OR BOTH. ALTERNATIVELY IT MAY ACTIVATE HLA CLASS II TRANSCRIPTION BY MODIFYING PROTEINS THAT BIND TO THE MHC CLASS II PROMOTER (BY SIMILARITY).
GNGYLQKMVSIS-DITSTYSSLLRYTCGSSVEA-TRAVMKHLAAVYQHGCLLGLSIAKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLTLNGLLQALQ--SPC-----IIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:108445; C2ta.
                                                                                          SVNEDVLLTTGLLCKYTAQRFKPKYKFFHKSFQEYTAGRRLSSLLTS-----HEPEEVTK
                                                                                                                                       TYMRHYFENSGTAGNQDKALGL ----
                                                                                                                                                                                 TTLFHTFYDLLIQKNKHKHKGVAASDFIRSLDHCGDLALEG-----VFSHKFDFELQDVS
                                                                                                                                                                                                                            CSLRGLLAGIFQRKLLRGCTLLLTARPRGRLAQSLSKAD-----AIFEVPSFSTKQAK
                                                                                                                                                                                                                                                                      -SAQALIREVLIKELAEG----LLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQ
                                                                                                                                                                                                                                                                                                                        LILDAFEELEAQD
                                                                                                                                                                                                                                                                                                                                                                 FLLDGYNEFKPQNCPEIEALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTED-
                                                                                                                                                                                                                                                                                                                                                                                                           VFYVPCHCLDRPGDTYHLRDLLCPPSLQPLAMDDEVLD-----YIVRQPDRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFFLR---LSRAQG--GLFETLC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLAHGGLAEVLQVVSDCRRPGETQVVAVLGKAGQGKSHWARTVSHTWA----CGQLLQYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U60653; AAB48859.1; -. U46562; AAB05004.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368
917
1078 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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375
917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 ATP (POTENTIAL).
17 G -> R (IN REF. 2).
118789 MW; 2BFEA61BBF581378 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 180.5; Db 1,
Pred. No. 0.0062;
""amatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene transfer of an EMT6 tumor that
                                             ----LSKALLEQGTEAQLPCTLTGLYVSLLGPAAQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DQLLDIPGTIRKQTFMAMLLKLRQRVL
                                                                                                                                       -----LEGQPLLCSYSH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barber J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               increase in tumor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bernstein R.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jolly D.,
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actinin in Dictyostelium discoideum.";
J. Cell Biol. 103:969-975(1986).
-!- FUNCTION: F-ACTIN CROSS-LINKING PR
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13-AUG-1987
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                      -!- SUBUNIT: HOMODIMER, A
-!- SIMILARITY: CONTAINS
-!- SIMILARITY: CONTAINS
-!- SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; NCBI_TaxID=44689;
                                                                                                                                                                                                                                "Calcium-sensitive non-muscle alpha-actinin structures and highly conserved regions."; FEBS Lett. 221:391-396(1987).
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Noegel A., Witke W., Schleicher M.;
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20-AUG-2001
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IS 1 ACTIN-BINDING DOMAIN.

IS 2 CALPONIN-HOMOLOGY DOMAINS (CH).

IS 2 EF-HAND CALCIUM-BINDING DOMAINS

IS 4 SPECTRIN REPEATS.
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SMART; SM00150; SPEC; 3.
SMART; SM00150; SPEC; 3.
PROSITE; PS00019; ACTININ_1; 1
PROSITE; PS00021; CH; 2.
PROSITE; PS00018; EF_HAND; 2.
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CONFLICT
SEQUENCE
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EMBL; X04324; CAA27855.1;
PIR; S00103; FADOAA.
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an email to license@isb-sib.ch).
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SPECTRIN 3.
SPECTRIN 3.
SPECTRIN 4.
EF-HAND 1 (BY SIMILARITY).
EF-HAND 2 (BY SIMILARITY).
T-> P (IN REF. 2).
T-> T (IN REF. 2).
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Pred. No. 0.0083;
7; Mismatches 33
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CH 1.
CH 2.
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09996; O9UQO4; Q9UQH3; O9Y66Y2; O14869; O43355; O94895; Q9Y6B8;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
A KINASE ANCHOR PROTEIN KINASE A ANCHORING PROTEIN 9) (PROTEIN KINASE ANCHORING PROTEIN 450 KDA) (AKAP 450) (A-KINASE ANCHOR PROTEIN 450 KDA) (AKAP 120 LIKE PROTEIN)
(HYPERION PROTEIN) (CGNTROSOME- AND GOLGI-LOCAL:
PKN-ASSOCIATED PROTEIN) (CGNTROSOME- AND GOLGI-LOCAL:
PKN-ASSOCIATED PROTEIN) (CGNTROSOME- AND GOLGI-LOCAL:
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MEDLINE-98151389;
    MEDLINE-99287934;
Takahashi M., Shil
                                                                                  TISSUE=Brain
                                                                                                                                                                                         "Cloning and characterization of a cDNA encoding protein located in the centrosome, AKAP450."; EMBO J. 18:1858-1868(1999).
                                                                                                                                                                                                                                                                                                                     Witczak O.,
Jahnsen T.,
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99219864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng "Yotiao, a novel protein of neuromuscular junction and brain that interacts with specific splice variants of NMDA receptor subunit
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                                                                                                                   SEQUENCE FROM N.A. (ISOFORM
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                                                                                                                                                                                                                                                                                                                     Skaalhegg B.S., Keryer
Oerstavik S.;
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        Shibata
                                             PubMed=10358086;
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A WU X., GRAVES T., BRADSHAW H.;

A WU X., GRAVES T., BRADSHAW H.;

L SUBMILTED (SEP-1998) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: BINDS TO TYPE II REGULATORY SUBUNITS OF PROTEIN KINASE AND R. SCAPFOLDING PROTEIN THAT ASSEMBLES SEVERAL PROTEIN KINASES AND C. S. SCAPFOLDING PROTEIN THAT ASSEMBLES SEVERAL PROTEIN KINASES AND C. EVENTS CAN BE REGULATED BY PHOSPHONYLATION STATE OF PROTEIN C. SUBSTRATES. I SOFORM 4/YOTIAO IS ASSOCIATED WITH THE N-METHYL-D-C. ASPARTATE RECEPTOR AND IS SPECIFICALLY FOUND IN THE NEUROMUSCULAR JUNCTION (NMJ) AS WELL AS IN NEUROMAL SYNAPSES EXPLAINING THAT ITS ROLE MAY BE TO ORGANIZE POSTSYNAPTIC SPECIALIZATIONS.

-!- SUBUNIT: INTERACTS WITH THE REGULATORY REGION OF PROTEIN KINASE N (PKN), PROTEIN PHOSPHATASE 1 (PP1)

C -1- SIDEUNITE NON-PHOSPHATASE 2A (PP2A), PROTEIN PHOSPHATASE 1 (PP1)

C -1- SIDEURITE NON-PHOSPHORYLATED FORM OF PKC EPSILON.
This SWI
between
the Eurc
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DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G., Trotter K.W., Milgram S.L., Goldenring J.R.; "AKAP350, a multiply spliced protein kinase A-anchoring protein associated with centrosomes."; J. Biol. Chem. 274:3055-3066(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of a novel giant scaffolding protein, CG-NAP, that anchors multiple signaling enzymes to centrosome and the golgi apparatus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2157-3911 FROM N.A. (ISOFORM TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kemmner W.A., Deiss S., Schwarz U.; "Cloning of Hyperion."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
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MEDLINE=99115654; PubMed=9915845;
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                                                           DOMAIN: RII BINDING SITE, PREDICTED TO FORM AN AMPHIPATHIC HELIX, COULD PARTICIPATE IN PROTEIN-PROTEIN INTERACTIONS WITH A COMPLEMENTARY SURFACE ON THE R-SUDULIT DIMER. CAUTION: REF. 6 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO TWO FRAMESHIFTS IN POSITIONS 3782 AND 3811.

CAUTION: REF. 9 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FOUR FRAMESHIFTS IN POSITIONS 29, 1653, 1699 AND 1735.
European
                                                                                                                                                                                           TISSUE SPECIFICITY: WIDELY EXPRESSED. ISOFORM 4/YOTIAO IS HIGHLY EXPRESSED IN SKELETAL MUSCLE AND IN PANCREAS.
                                                                                                                                                                                                                                                                CYTOPLASMIC ALTERNATIVE
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              SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                              4/YOTIAO,
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PRODUCTS: 6 ISOFORMS; 1
AO, 5 AND 6/AKAP350; ARE
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spliced family of proteins with centrosomal
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LQAVSESTVPPSLPVDSVVITESDAQRTMYPGSCVKKNIDGTIEFSGEFGVKEETNIVKL
                                                                                                                                                                                                                                                                        E----SLQSVKNTTEQEILKAININSFVECG-----IHLYQESTSKSALSQEFEAFFQGK
                                                           TNLEDIDVNHKSKLSSLQDLEKTKLEEQVQELESLISSLQQQLKETEQNYEAEIHCLQKR
                                                                                                                         YNKLLVLQTRLSKIW---GQQTDGMKLEFGEEN-LP-----
                                                                                                                                                        FIKLDFYGGAMAS-WEKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDF
                                                                                                                                                                                        CSVLGEYYTPALKCEVNAEDKENSGDYISENEDPELQDYRYEVQDFQENMHTLLNKVTEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVGDMTEDS - - AQALIREVLIKELAEGLLLQIQKSRCLRNLMKTPLF - - - - VVITCAIQM
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                                                                                                                                                                                                                                                                                                                                                 STYSSL-----LRYTCGSSVEATRAVMKHLAAVYQHG------CLLGLSIAKRPLWRQ
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                                                                                          SKLNKQDITYLGKIFS----SATSLRLQIKRCAGVAGSLSLVLSTCKNIY-----
                                                                                                                                                                                                                                                   EEKIKELQKI-HQLELQTMKT-----QETGDEGKPLHLLIGKLQK-AVSEECSYFLQTL
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> S (IN REF. 3).
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between
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P28025;
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MOL. Cell. Biol. 11:3395-3398(1991).
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01-AUG-1992 (Rel. 23, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
KINESIN-RELATED MOTOR PROTEIN EGS 1.
                                           PIR; A40264; A40264.
                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                    modified
                                                                                                                                                      use
                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1665
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                                                                                                                                                                                                                                                                                                                                                                           ESTABLISHING A BIPOLAR SPINDLE. ASSOCIATES WITH BOTH INTERPHASE AND SPINDLE MICROTUBULES. MAY BE INVOLVED IN NUCLEAR DIVISIONS TAKING PLACE DURING THE DEVELOPMENT OF UNFERTILIZED EGGS.

TAKING PLACE DURING THE DEVELOPMENT OF UNFERTILIZED EGGS.

SUBUNIT: HETEROTETRAMER OF TWO HEAVY AND TWO LIGHT CHAINS.

SUBUNIT: LOCATION: CONCENTRATED AROUND THE POLAR ENDS OF BOTH MEIOTIC AND MITOTIC SPINDLES.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN UNFERTILIZED EGGS,
                                                                                                                                                                                                                                                     SOON AFTER FERTILIZATION.

SOON AFTER FERTILIZATION DURING MITOSIS AT THR-930 CONTROLS THE PTM: PHOSPHORYLATION DURING MITOSIS AT THR-930 CONTROLS THE ASSOCIATION OF EGS WITH THE SPINDLE APPARATUS (BY SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. BIMC
                                                                                                                                                                                                                                                                                                                            CHANNELS. ALSO PRESENT IN TESTIS. DEVELOPMENTAL STAGE: EGG MATURATION.
                                                                                                                                                                                                                                                                                                                                                              ESPECIALLY IN THE GERMINAL VESICLE AND
                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                               X54002; CAA37950.1;
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and this statement
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SMART; SMO0129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1;
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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QLNLLGMETQQQFSGFLSKGGKLQKSVGSLQQDLDLVSSEAIECISSHHKKLAEQSQDVA
                                                                                                                                                                                                                                                                                                                                                              SRCLRNLMKTPLFVVITCA--IQMGESEFHSHTQTTLFHTFYDLLIQKNKHKHKGVAASD
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                         -----VTLRDFS-----KLNK-----QDITYLG---
                                                                                  AMASWEKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLE:

    SQAKGDLQQLMAAHRTGLEEALRSDLLPVVTAVLDLNSHLSHCLQNFLIVADKIDSHKE

                                                                                                                                       ESTSKSALSQEFEAFFQGKSLYINSGNIP--DYLFDFFEHLPNCASALDFI--KLDFYGG
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                                                                                                                                                                                                                                                SFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMV-SISDITSTYSSLLRYTCGSSVEATR
                                                                                                                                                                                                                                                                               FVVSAFETTEKKLHGT-ANKL-----LSTVRETTRDVSGLHEKLDRKKAVDQHNFQVHE
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                                                     -FTEHSRSLHKLRLDSSSALSSIQSEYESLKEDIATAQSMHSEGVNNLISSLQN
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ATP-binding; Coiled coil; Mitosis;
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SPCA_HUMAN SIALL.

P02549; Q15514;

21-JUL-1986 (Rel. 01, Created)

1 01-NOV-1995 (Rel. 32, Last seque

T 15-JUL-1999 (Rel. 38, Last anno'

T ATTERN ALPHA CHAIN, ERYTHROCY
Sahr K.E., Tobe T., Scarpa A., Laughinghouse K., Marchesi S Agre P., Linnenbach A.J., Marchesi V.T., Forget B.G., "Sequence and exon-intron organization of the DNA encoding I domain of human spectrin. Application to the study of mut causing hereditary elliptocytosis.";
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                                                                                                                                                                                                                                                                                                                                                                                                      "The complete cDNA and alpha-spectrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90170949; PubMed=1689726;
Sahr K.E., Laurila P., Kotula L.,
Linnenbach A.J., Winkelmann J.C.,
                                                                                                                                                                                                        alpha-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Curtis P.J., Forget B.
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Eukaryota; Metazoa; (
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Primates;
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Speicher D.W., Marchesi
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V.T.,
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WARIANT VAL-1857.

MEDLINE=93253053; PubMed=8486776;

Wilmotte R., Marechal J., Morle L.,

Kastally R., Kotula L., Delaunay J.,

"Low expression allele alpha LELY of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coetzer T.L., Sahr K., Prchal J., Blacklock H. Doyle J., Manaster J., Palek J.;
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                                                                                                                                                                                                                           Lecomte M.-C., Garbarz M., Grandchamp B., Feo C. Devaux I., Bournier O., Galand C., D'Auriol L., Sahr K.E., Forget B.G., Boivin P., Dhermy D.; "Sp alpha I/78: a mutation of the alpha I spectr kindred with HE and HPP phenotypes."; Blood 74:1126-1133(1989).
                                                                                                                                                                                                                                                                                                                                                             "Heterogeneity of the molecular be pyropoikilocytosis and hereditary increased levels of the spectrin peptide.";
                                                                                                                                                                                                                                                                                                                                           peptide.";
Blood 78:1364-1372(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91346849; Pub
Floyd P.B., Gallagher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91358728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of three novel spectrin alpha I/74 mutations hereditary elliptocytosis: further support for a triple-strar folding unit model of the spectrin heterodimer contact site."
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Maillet P., Alloi:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-84295638; PubMed-6472478; Speicher D.W., Marchesi V.T.;
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"Erythrocyte spectrin is comprised
                                                                                                  common type of the spectrin alpha I 46-50a-kD peptide abnormality hereditary elliptocytosis and pyropoikilocytosis is associated tha mutation distant from the proteolytic cleavage site. Evidence r the functional importance of the triple helical model of
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yher P.G., Valentino
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sio N., Morle L.,
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Palek J.,
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"Spectrin Anastasia (alpha I/78): a new spectrin Arg-->Thr) with moderate elliptocytogenic potent: Br. J. Haematol. 89:933-936(1995).
-i- FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT
                                                                                                                                                                                                                                Perrotta S., del Giudice E.M., Alloisio N., Delaunay J., Cutillo S., Lolascon A.; "Mild elliptocytosis associated with the algin spectrin Genova (alpha 1/74).";
                                                                                                                                                                                                                                                                                                                                               "Spectrin Tunis (Sp alpha I/78), an elliptocytogenic
to the CGG->TGG codon change (Arg-->Trp) at position
alpha I domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with elliptocytosis and the dimer self-association site.";
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Morle F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93372367; PubMed=8364215; dalla Venezia N., Alloisio N., Forissier A., Denoroy L., Vives-Corrons J.L., Besalduch J., Besson I., Delaunay J., "Elliptopoikilocytosis associated with the alpha 469 Hismutation in spectrin Barcelona (alpha I/50-46b)."; Blood 82:1661-1665(1993).
                                                                                                                                                   Cutillo
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                                                                                                                                                               Perrotta S.,
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Ducluzeau M.-T., Denor
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MEDLINE=94043025;
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FUNCTION: SPECTRIN IS THE MAJOR CONSTITUENT OF THE CYTOSKELETAL RETWORK UNDERLYING THE ERYTHROCYTE PLASMA MEMBRANE. IT ASSOCIATES WITH BAND 4.1 AND ACTIN TO FORM THE CYTOSKELETAL SUPERSTRUCTURE OF THE ERYTHROCYTE PLASMA MEMBRANE.

SUBUNIT: COMPOSED OF NONHOMOLOGOUS CHAINS, ALPHA AND BETA, WHICH AGGREGATE SIDE-TO-SIDE IN AN ANTIPARALLEL FASHION TO FORM DIMERS, TETRAMERS, AND HIGHER POLYMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INE-90347052; PubMed=2384601;
e L., Roux A.-F., Alloisio N., Pothier B., Starck J., Denorce E., Rudigoz R.-C., Forget B.G., Delaunay J., Godet J.;
elliptocytogenic alpha I/74 variants of the spectrin alpha in. Spectrin Culoz (GGT-->GTT; alpha I 40 Gly-->Val) and trin Lyon (GTT-->TTT); alpha I 43 Leu-->Phe).";
lin. Invest. 86:548-554(1990).
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lin. Invest. 91:2091-2096(1993)
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83:3346-3349(1994).
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74:828-832(1989).
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                                                                                                                                                a S., Iolascon A., de Angelis S., del Giudice E.M.;
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                                                             ---IKYSTIGLAQQW-----DQLYQLGLRMQHNLEQQIQAK----
                                                                                              HNLVKLSILDLSENYLEKDGNEALHELIDRM--NVLEQLTALMLPWGCDVQG-----S
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BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM),
DOMAIN (M),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
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Gentles S., Bowman S., Barrell B.G., Rajandrea Submitted (MAY-1995) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.
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P49454; Q13246; Q13171;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seque
20-AUG-2001 (Rel. 40, Last annot
CENP-F KINETOCHORE PROTEIN (CENT
                                                                    Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., (Jones D., Yang-Feng T.L., Lee W.-H.; "Characterization of a novel 350-kilodalton nuc that is specifically involved in mitotic-phase Mol. Cell. Biol. 15:5017-5029(1995)
                                                                                                                                                                                                                                                                                        TISSUE-Breast carcinoma;
MEDLINE-95348175; PubMed-7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Y
"CENP-F is a protein of the nuclear matrix that
kinetochores at late G2 and is rapidly degraded
J. Cell Biol. 130:507-518(1995).
                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=95379848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                    SEQUENCE OF 2194-3210 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-95336446;
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Similarity

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Score Pred.

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"Characterization of the kinetochore binding domainteractions with the kinetochore proteins CENP-F
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SUBUNIT: HOMO- OR HETERODIMER.
SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN T
SUBCELLULAR LOCATION: NUCLEAR MATRIX (BUT NOT IN T
REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORC
THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.
DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING
PTM: HYPERPHOSPHORYLATED DURING MITOSIS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: GTPASE-ACTIVATING PROTEIN (GAP) FO INVOLVED IN THE CONTROL OF CELLULAR MORPHOGE PROPER BUD SITE SELECTION AND BUD EMERGENCE.
-!- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 1 GAP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ploidy mutants in yeast.";
Genetics 135:677-691(1993).
-!- FUNCTION: GTPASE-ACTIVE
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo Dietrich F.S., Mulligan J.T., Carpenter J., Chen E., Cherry Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Chung E., Lashkari D., Lew H., Lin D., Chen H., Lin D., Chen M., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Chen M., Chen
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"Control of cellular morphogenesis by the Ip12/Bem2
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
GTPASE ACTIVATING PROTEIN BEM2/IPL2.
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                                                                     EMBL; U18917; AAB64682.1; SGD; S0000957; BEM2.
                                                                                                                                           EMBL; Z35159; CAA84524.1; -. EMBL; L33832; AAA57132.1; -.
                                                                                                                                                                                                                                                  or send an email to
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J. Cell Biol. 127:1395-1406(1994).
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                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed
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Peterson J., Zheng Y., Bender L.,
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                                                                                                                                                                                                                                              equires a license agreement (S email to license@isb-sib.ch).
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nes 205; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNSRALIQRMGMTVIKQITDDLF-VWN--VLNREEVNIICCEKVEQDAARGIIHMILKKG 62
CGSSVEATRA--
                                                                                                                                                                                                                                                                                                                                                                             TLNGLLQALQ-----SPCIIEGESGKGK---STLLQRIAMLWGSGKCKALTKFKF 199
                         ---LHQAVPK--KNRKSVIISGTHSDNDHSYNINKNTGQTPSLGSVME--SNNSARNRRD 1809
                                                                                                      VAASDFIRSLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTAQRFKPK 438
                                                                                                                                  NIISNVLDLIPNEREFPLDIEM -- SDENPSKRTTFGRILFNNFEDV -- -- NKVYRKKTKK 1706
                                                                                                                                                                                                                                        ICPHIPAFIETAIAHAIISPESRNYELSWIKASEKLSDPTKGTQNLRSISNVLEKIDDIH
                                                                                                                                                                                                                                                                                             FFVMEISNVNKSSSERLTTCKVILQILNYIR-----WKNGSLDLFDSEEDESPHA 1536
                                                                                                                                                                                                                                                                                                                      VFFLRLSRAQGGLFE--TLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFKPQN 257
                                                                                                                                                                                                                                                                                                                                                  INPGYLQLHEFEISNLFTWISTLILKDDNGTESLFFEKLPQSIKLL-----IKLHTSLTT 1486
                                                                                                                                                                                                                                                                                                                                                                                                      STNYEDILEWIYQLDNFISKKFNLVSKKDWIVLFQELELLSKESLVSFFNYPLHFKSSKL 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGIKSAYQKQLYRPIGVNRTQKRITDILNSFNTFSFTDLNNIIDDPSFSDDMIRSFQKLH 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S----ESCN--LFLKSLK-----EW-----NYPLFQDLNGQ-------SLF
                                                                              VSESEAISE-
                                                                                                                                                          NLMKTPLFVV----ITCAIQMGESEFHSHTQTT----LFHTFYDLLIQKNK---HKHKG
                                                                                                                                                                                      IKRF----IEIDDVFSKNCKNLCPCPGWFISRLLEISQFVPNMSITNSKLINFDKRRFVN 1652
                                                                                                                                                                                                               IRQFGALTAEVGDMTEDSAQALI-----REVLIKELAEGL-----LLQIQKSRCLR 332
                                                                                                                                                                                                                                                                    PS50003;
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POLY-ASN.
POLY-SER.
POLY-THR.
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POLY-SER.
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RESULT 15
YBA4_YEAST
ID YBA4_YEAST
AC P35194;
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CONFLICT
                                                                                      EMBL; Z35765; CAA84821.1;
EMBL; Z26494; CAA81266.1;
PIR; S45734; S45734.
                                                                         PIR; S45734; S45734.
SGD; S0000100; YBL004W.
                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                               use
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                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                   Yeast 10:S41-S46(1994)
                                                                                                                                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                               Wolfe K.H., Lohan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 287.5 KDA PROTEIN IN PDR3-HTA2 INTERGENIC
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 SEQUENCE
                                             Hypothetical protein; TRANSMEM 1170 118
                                                                                                                                                                                                                                                                                                                "Sequence around the centromere of chromosome II: similarity of CEN2 t
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94378721; PubMed=8091860;
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1214-2493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNLKNLTKLIMDNIKMNEEDAIKLAEGLKNLK-----KMCLFHL--THLSDIGEGMD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNGHEYLIQTASSSDLTEWIKMIKASKRFSFHSKKYKG--KTHNKIFGVPLEDVCERENT
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1480 16
2440 24
2493 AA;
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POTENTIAL.
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MW; A7EC4E3E9AE132B3 CRC64;
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              CAA84821).
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                                                                                                                                                                                    689 ---YTKDEALVWKL--VLS 702
                             974 TKEELPDPALVRKLSQVLS 992
                                                                                            645 VGAEFGKTKT------DKLVSSFFLKYLFGLLTVRFSPVWTGVFDTLPNV----- 688
                                                                                                                                                                                                                                                                                                                                                                                                      747 QNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHLSDIGE 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 NKITILIERIMSQSENCASLSQDKVAFLFALFIRNSDVKTLTLFHQKLFNYALTNISDCF 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 ----LLPVYE------VMYQDFNDSLDATNIDRILKVLTTIVFSESGRKIPDW 333
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                                                                                                                     927 LGAFFGKNPLKNEQQLNLAGNRVSSDGWLAFM-------GVFENLKQLVFFDFS 973
                                                                                                                                                                                                                                                                                    560 -----KLVSNLHPSESLKGLMSHYPSL----LLSLTDNFMLPDGK- 595
                                                                                                                                                                                                                                                                                                                        807 GMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSENYLEKDGNE 866
                                                                                                                                                                                                                                                                                                                                                                            529 ED------DASGN--NLLKTILDNYE-NYKESLNFLRGWN------ 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 S---KLQ-----NTEITIPLLERIFSTF--ASPDNFTKDMVGT-----LLKIYRK 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   687 ATSLRLQIKRCAGVAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKTLSIHDL 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 IALFFLEVDDKPELQKVREVNFPEEF---ILSIRDFFVTAEINDSNDLFEIYWRAIFKY 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                649 VSLFF------NWKQEFRTLEVTLRDF---SKLNKQ----DITYLGKIFSS 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 LEFFQF----ALRLSYERVFSFNGLKFLQLFLKKNWQS-------QGKK 431
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Search completed: March 25, 2002, 11:00:19 Job time: 239 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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US-09-697-089-2
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd
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sp_bacteria:*
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11 Q9ZLM5
11 Q9JLM5
11 Q9JLC29
4 Q9HC29
4 Q9HT4
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4 Q9YZE0
4 Q9YZE0
4 Q9BZB
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4263.674 Million cell updates/sec
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Q9y239 homo sapien
Q9h6g6 homo sapien
Q9hx02 homo sapien
Q9bvn5 homo sapien
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Q9hc29 homo
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for ir
human gene transcripts.";
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Pluvinet R., Estivill X., Escarceller M., Sumoy L.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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706 LVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKTLSIHDLQNQRLPGGLTDSLGNLKNL 765
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                                                                         SRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDIRYLGKIFSSATSLRLQIKRCAGVAGSLS 120
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AB Bertin J., Nir W.-J., Fischer C.W., Tayber O.V., Errada P.R.,

AGrant J.R., Keilty J.J., Gosselin M.L., Robison K.E., Wong G.H.W.,

Glucksmann M.A., DiStefano P.S.;

"Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member

that activates NF-kappaB.";

"Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member

that activates NF-kappaB.";

"Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member

that activates NF-kappaB.";

"Human CARD4 protein is a novel CED-4/Apaf-1 cell death family member

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                                                                 Query Match 5.6%;
Best Local Similarity 20.8%;
Matches 240; Conservative 15
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Q9Y239;
01-NOV-1999
01-NOV-1999
01-JUN-2001
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MEDLINE-99262599; PubMed-10329646;

Inohara N., Koseki T., del Peso L., Hu Y., Ye

Merino J., Liu D., Ni J., Nunez G.;

"Nod1, an Apaf-1-like activator of caspase-9

kappaB.";
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153; Mismatches
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                                                                                                                                                                                                                                   DNNNLNDYGVRELQPCFSRLTVLRLSVNQITDGGVKVLSEELTKYKIVTYLGLYNNQITD
                                                                                                                                                                                                                                                                                                                               DFSKLNKQDITYLGKIFSSATSLRLQIKRCA-GVAGSLSLVLSTCKNIYSLMVEASPLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGLLCKYTAQRFKPK-----YKFFH------KSFQEY- 449
                                                  LLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPLKN---FQQLNLAGNRVSSDGWL
                                                                                                                       ILAQNIHNIVKLSIIDISENYIEKDGNEALHELIDRMNVLEQLTALMIPWGCDVQGSLSS
                                                                                                                                                            VKNSKS-----
                                                                                                                                                                                              LKNLKKMCLFHLTHLSDIG-----EGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVK
                                                                                                                                                                                                                                                      EDERHITSYTNLKTLSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEG
                                                                                                                                                                                                                                                                                                                                                                                                               LDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSR-AVSLFFNWKQEFRTLEVTLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPAGAATTSCYPPFLPFQCLQGSGPAREDLFKNKDHFQFTNL--FLCGLLSKAKQKLLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QRNTRSPVETLHAG----RDTLCSL----GQVAHRGMEKSLFVFTQEEVQASGLQERDMQL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKNKHK-----HKGVAASDFIRSLDHCGDLALEGVFSHKFDFELQDV--SSVNE-DVLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCSLCSVPLFCWIIFRC-FQHFRAAFEGSPQLPDCTMTLTDVFLLVTEVHLNRMQPSSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRNLMKTPLF--VVITCAIQMGESEFHSHTQ-----TTLFHTFY------DLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASKLLTARTG--IEVPRQFLRKKVLLRGFSPSHLRAYARRMFPERALQDRLLSQLEANPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAGVKFFFHFRCRMFSCFKESDRLCLQDLLFKHYC----YPERDPEEVF-AFLLRFPHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KALTKEKEVEELRLSRA------QGGLEETLCDQLLDIPGTIRKQTEMAMLLKLRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELVGFSNESLGSLNSLACLLDHTTGILNEQGETIFILGDAGVGKSMLLQRLQSLWATGRL
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                                                                                     SLARALQQNTSLEILWLTQNELNDEVAESLAEML-
                                                                                                                                                                                                                                                                                                                                                                                LSFV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVPA----AALRRKRKALWAHLFSSLRGYLKS-----LPRVQVESFNQVQAMPTFIWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLRYTCGSSVEATRAVMKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALFTFDGLDELHSDLDLSRVPDSSCPWEPA-----HPLVLLANLLSGKLLK-----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYPLGEDIDIIFNLKSTFTEPV-LWRKDQHHH------RVEQLTL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QSKVVVN----TDPVSRYTQQLRHHLGRDSKFVLCYAQKEELLLEEIYMDTIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGLLQALQS-PCIIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- RALPELGPGGDQQSYEFFHLTLQAFFTAFFLVLDDRVGTQELLRFFQEWM
                                                                                                                                                            -ISEVGMWGNQVGDEGAKAFAEALRNHP-SLTTLSLASNGISTEGGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---KPQNCPEIEALIKENHRFKNMVIVTT--TTECLRHIRQFG
              -W-LIQNQITAKGTAQLADALQSNTGITEICLNGNLIKPEE--
                                                                                                                                                                                                                                                                                                                                                                              ---H.J--
                                                                                                                                                                                                                                                                                                                                                                              ----HFPKRLALDL--
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                                                                                     ---KVNQ
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Best Local Similarity
Matches 201; Conserv
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*NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ dai EMBL; AK025992; BAB15293.1; -.
InterPro; IPR003592; LRR_out.
InterPro; IPR003592; LRR_out.
InterPro; IPR003592; LRR_RNInh.
InterPro; IPR003592; LRR_RNInh.
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SMACH; SM00370; LRR; 7.
SMART; SM00368; LRR_RI; 8.
SEQUENCE 1062 AA; 120488 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                    LR-----YTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWR------
                                                                                                                                                                                                                      TAQRFKPKYKFFHXSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSL 490
QVIKENLPENVTASESDAEVERSQDDQHMLPFWTDL--CSIFGSNKDLMGLAINDSFLSA
                                 YINSGNIPD-----
                                                                STYTDLQELLGCLYESQEEELVKEV-MAQFKEISLHLNAVDVVPSSFCVKHCRNLQKMSL
                                                                                                                                 ERLRNPDLIQAGYYSFGLANE-KRA--KELEATF--GCRMSPDI-KQELLRCDISCKGGH
                                                                                                                                                                                                 RVS--KGCYSFIHLSFQQF-----LTALFYTLEKEEEEDRDGHTW---DIGDVQKLLSGV
                                                                                                                                                                                                                                                                                     HKHKGVAASDFIRSLDHCGDLALEGVFS-----HKFDFELQDVSSVNEDVLLTTGLLCKY 430
                                                                                                                                                                                                                                                                                                                                                                                                      NRVMLPKAALLVTTRPRALRDLR----ILAEEPIYIRVEGFLEEDRRAYFLRHFGDEDQA
                                                                                                                                                                                                                                                                                                                                                                                                                                     KENHRFKNMVIVTTTTECLRHIRQFGALTAE------VGDMTEDSAQALIREVLIKELA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WP---ELQDDIPHILAQARKILFVIDGFDELGAAPGALIEDSCGDWEKKKPVPVLLGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFK------PQNCPEIE------ALI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFL---RLSRAQGGLFETLCDQLLD
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                                                                                                                                                                                                                                                                                                                                    MRAFELMRSNAALFQLGSAPAVCWIVCTTLKLQMEKGEDPVPTCLTRTGLFLRFLCSRFP
                                                                                                                                                                                                                                                                                                                                                                   EGLLLQIQKSRCLRNLMKTPLFVVITCA---IQMGESEFHSHTQTTLFHTFYDLLIQKNK 375
                                                                                                                                                                                                                                                                  -QGAQLRGALRTLSL----LAAQGLWAQTSVLHREDLERLGVQESDLRLFLDGDILRQD
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                                                                                   -QESLQSVKNTTEQEILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSL
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                                 -----YLFDFFEHLPNCA---SALDFIKL----DFYGG
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Shibahara T., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337;
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                                                                                                     Query Match
Best Local Similarity 22.5
Matches 201; Conservative
                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBa Submitted (FEB-2001);
EMBL; AK000517; BAA91223.1; -.
EMBL; AF310106; AAG30289.1; -.
EMBL; BC003592; AAH03592.1; -.
InterPro; IPR000767; Disease_resist.
InterPro; IPR0037592; IRR_out.
PRINTS; PR00364; DISEASERSIST.
SMARP; SM00370; LRR; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09NX02;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tash: Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ database: Submitted (FEB-2000)
                                                                                                                                                                                                                                          Hypothetical SEQUENCE 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence up
01-CUT-2001 (TrEMBLrel. 17, Last annotation
NALP2 (HYPOTHETICAL 120.5 KDA PROTEIN).
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VLYGPAGLGKTTLAQKLMLDWAED--NLIHKFKYAFYLSCRELSRLGPCSFAELV--FRD
                                    IIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFL---RLSRAQGGLFETLCDQLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLWL-WGCSIPPFSCEDLCSALSCNQSLVTLDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHL----SDIGE-GMDYIVKSLSSEPCDL 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTLVLWNCDITSDGCCDLTKLLQEKSSLLCLDLGLNHIGVKGMKFLCEALRK--PLCNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSLENCHLTEANCKDLAAVLVVSRE-----LTHLCLAKNPIGNTGVKFLCEGLRYPECKL
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                                                                                                                                                                                                                                       al protein.
1062 AA; 120514 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARCINOMA;
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', LRR and PYD containing |
to the EMBL/GenBank/DDBJ
                                                                                                                                    5.0%;
22.5%;
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                                                                                                           123;
                                                                                                     Score 264; DB 4;
Pred. No. 3.4e-09;
3; Mismatches 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                            Q9BVN5 PRELIMINARY; PRT; 1062 AA.
Q9BVN5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 120.6 KDA PROTEIN.
                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Euthoria; Primates;
MCDI_TaxID=9606;
      SEQUENCE FROM N.A.
TISSUE=CHORIOCARCINOMA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGNDQDDMFPALCEVLRHPECNLRYLGLVSCSATTQQW-----ADLSLALEVNQSL
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                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
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Submitted (DEC-2000) to the EMBL; BC001039; AAH01039.1;
Hypothetical protein.
SEQUENCE 1062 AA; 120572
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958
                            883 ALMLPWGCDVQG-SLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPL
                                                                                                                                      LIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHL----SDIGE-GMDYIVKSLSSEPCDL
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                                                            QTLVLWNCDITSDGCCDLTKLLQEKSSLLCLDLGLNH1GVKGMKFLCEALRK--PLCNLR
                                                                                        EEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSENYLEKDGNEALHELIDRMNVLEQLT
                                                                                                                       LSLENCHLTEANCKDLAAVLVVSRE-----LTHLCLAKNPIGNTGVKFLCEGLRYPECKL
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                                                                                                                                                                                                                                                                                                        SLVRILCEQIASDT--CHLQ------RVVFKNISPADAHRNLCLALRGHKTVTYLTL
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                                                                                                                                                                                                                                                                                                                                     AMAS -- WEKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKL -- -- -
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Similarity 22.5%;
O1; Conservative 12:
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WGCSIPPFSCEDLCSALSCNQSLVTLDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                            -QESLQSVKNTTEQEILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSL
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Pred. No. 3.4e
23; Mismatches
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3.4e-09;
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Best Local Similarity 22.5%;
Matches 201; Conservative 13
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01-JUN-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NUCLEOTIDE-BINDING SITE PROTEIN 1.
Homo saptens (Human).
Eukaryota: Materia
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SMART; SM00370; LRR; 6.
SMART; SM00368; LRR_RI; 8.
SEQUENCE 1033 AA; 117387 MW;
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Mammalia; Eutheria; Primates;
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InterPro; IPR003590; LRR_RNinh.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLYGPAGLGKTTLAOKLMLDWAED--NLIHKFKYAFYLSCRELSRLGPCSFAELV--FRD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFL---RLSRAQGGLFETLCDQLLD
                                                                                                                                                                                                                                                                                                                 TAQRFKPKYKFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSL 490
                                                                                                                                                                                                                                                                                                                                                                          HKHKGVAASDFIRSLDHCGDLALEGVFS-----HKFDFELQDVSSVNEDVLLTTGLLCKY 430
                                                                                                                                                                                                                                                                                                                                                                                                                         MRAFELMRSNAALFQLGSAPAVCWIVCTTLKLQMEKGEDPVPTCLTRTGLFLRFLCSRFP
                   --NKQD--
                                                                                                          QVIKENLPENVTASESDAEVERSQDDQHMLPFWTDL--CSIFGSNKDLMGLAINDSFLSA
                                                                                                                                                                      STYTDLQELLGCLYESQEEELVKEV-MAQFKEISLHLNAVDVVPSSFCVKHCRNLQKMSL
                                                                                                                                                                                                                                  ERLRNPDLIQAGYYSFGLANE-KRA--KELEATF--GCRMSPDI-KQELLRCDISCKGGH
                                                                                                                                                                                                                                                    LR------YTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWR------
                                                                                                                                                                                                                                                                                              RVS--KGCYSFIHLSFQQF-----LTALFYTLEKEEEEDRDGHTW---DIGDVQKLLSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGLLLQIQKSRCLRNLMKTPLFVVITCA---IQMGESEFHSHTQTTLFHTFYDLLIQKNK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRVMLPKAALLVTTRPRALRDLR----ILAEEPIYIRVEGFLEEDKRAYFLRHFGDEDQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KENHRFKNMVIVTTTTECLRHIRQFGALTAE-----VGDMTEDSAQALIREVLIKELA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WP---ELODDIPHILAQARKILFVIDGFDELGAAPGALIEDICGDWEKKKPVPVLLGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPGTIRKQTFMAMLLKLRQRVLFLLDGYNEF-------KPQNCPE-IEALI 265
                                              SLVRILCEQIASDT - - CHLQ - - - - - -
                                                                            AMAS - - WEKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKL - - - - -
                                                                                                                                                                                                                                                                                                                                                          -QGAQLRGALRTLSL---LAAQGLWAQTSVLHREDLERLGVQESDLRLFLDGDILRQD
                                                                                                                                                                                                   QESLQSVKNTTEQEILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSL
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Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       %; Score 261.5; DB 4;
%; Pred. No. 4.8e-09;
123; Mismatches 336;
                -ITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Motif
                                                                                                                                      ----YLFDFFEHLPNCA---SALDFIKL----DFYGG
=
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Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C16152AD510BCA63 CRC64;
                                              RVVFKNISPADAHRNLCLALRGHKTVTYLTL
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Best Local S
Matches 210
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Q9R1M5;
Q9R1M5;
Q9R1MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOPH....
MATER OR OP1.
Mus musculus (Mouse).
Mus musculus (Metazoa; Chordata;
"heria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                  Tong Z.-B., Nelson L.M.;
"A mouse gene encoding an oocyte antigen premature ovarian failure.";
Endocrinology 0:0-0(1999).
EMBL; AF074018; AAD51762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OOPLASM SPECIFIC MATER OR OP1.
                                                                                                                                                                                                                                                                                         Pfam; PF00560; LRR; 2.
PRINTS; PR00366; DISASERSIST
SMART; SM00370; LRR; 7.
SEQUENCE 1111 AA; 125501 MV
                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1345193; Mater.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=NIH/SWISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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             335
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                                                            292
                                                                                                                                                                                                                               Local Sinhes 210;
                                                                                                                                                                                              DQHHHRVEQLTLNGLLQALQS-----PCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKF
                                                                                                                                   SFVIFFSVREIKWTEKSSLAQ - - LIAKECPDSWDLVTKIMSQP -
                                                                                                                                                                               CLWL-WGCSIPPFSCEDLCSALSN-QSLVTLDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTLVLWNCDITSDGCCDLTKLLQEKSSLLCLDLGLNHIGVKGMKFLCEALRK--PLCNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHL----SDIGE-GMDYIVKSLSSEPCDL
                                                                                                         GYN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALMLPWGCDVQG-SLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSLENCHLTEANCKDLAAVLVVSRE-----LTHLCLAKNPIGNTGVKFLCEGLRYPECKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCVNLSDNELLDEGAKLLYTTLRHPKCF
                                                                                                                                                         KFVFFL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSENYLEKDGNEALHELIDRMNVLEQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCKNI---YSLMVEASPLTIEDERHITSVTNLKTLSIHDLQNQRLPGGLTDSLGNLKNLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGNDQDDMFPALCEVLRHPECNLRYLGLVSCSATTQQW-----ADLSLALEVNQSL
                                                           ALTAEVGDMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNL--
                                                                                   GLDDMDSVLQHDDMTLSRDWKDEQPIYILMYSLLRKALLPQSFLIITTRNTGLEKLKSM-
                                                                                                                                                                                                                              Similarity 20.(
10; Conservative
           -MKTPLFVVITC-AIQMGES----EFHSHTQTTLFHT--FYDLLIQKNKHKHKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last seq
(TrEMBLrel. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN.
                                                                                                        ----EFKPQNCPEI--EALIKENHRFKNMVIVTTTTECLRHIRQFG
                                                                                                                                                  -RLSRAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLD
                                   -VVSPLYI---LVEGLSASRRSQLVLENISNESDRIQVFHSLIENH
                                                                                                                                                                                                                                         4.6%;
                                                                                                                                                                                                                                                                                           125501 MW;
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Pred.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                               ore 242; DB 11;
ed. No. 1.1e-07;
Mismatches 395
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on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murinae;
                                                                                                                                   -ERLLFVID
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RESULT
Q9JLR2
ID Q92
AC Q92
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Q9JLR2;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-UN-2001 (TrEMBLrel. 17, Last annotation updat
MATERNAL-ANTIGEN-THAT-EMBRYOS-REQUIRE PROTEIN.
   SEGGUENCE FROM N.A.
STRAIN=129/SV; TISSUE=OOCYTE;
MEDLINE=2022768; PubMed=10754103;
Tong Z.B., Nelson L.M., Dean J.;
                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1021
                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                JEAN.
JER.

Is musculus (Mouse).

Is musculus (Mouse).

Is musculus (Mouse).

Is musculus (Mouse).

Is musculus (Mouse).
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R InterPro; IPR003592; LRR_out.

Pfam; pF00560; LRR; 2;

PRINTS; pR00364; DISEASERSIST.

SMART; SM00370; LRR; 7.

SEQUENCE 1111 Ax.
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                                                                                                                                                                                                                                                                           CGIHLYQESTSKSALSQEFEAFFQGKSLYINSG---NIPDYLFDFFEHLPNCASALDFIK
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                                                                  VDIRD--LLSVDNTLELCPVVTVQE-----TQCKPLLMEWWGNFCSVLGSLRNLKELD
                                                                                                                                LDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKLN
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No. 1.3e-07;
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                                                              Query Match
Best Local Similarity
Matches 214; Conserv
                                                                                                                                    J. Biol. Chem. 0:0-0(2001).

EMBL; AF178930; AAG33677.1; -.

InterPro; IPR001687; ATP_GTP_A.

InterPro; IPR001315; CARD.

InterPro; IPR001611; LRR.

InterPro; IPR003592; LRR_Out.

InterPro; IPR003590; LRR_RNinh.

Pfam; PF00560; LRR; 2.

SMART; SM00370; LRR; 5.

SMART; SM00370; LRR; 5.

SMART; SM00370; LRR, 1; 7.

PROSITE; PS50209; CARD; 1.

SEQUENCE 1040 AA; 115282 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9HC29 PRELIMINARY;
O9HC29;
O1-MAR-2001 (TrEMBLrel. 16,
O1-MAR-2001 (TrEMBLrel. 17,
O1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                            Ogura Y., Inohara N., Benito A., Chen F.F., Yamaoka S., "Nod2, a Nod1/Apaf-1 family member that is restricted to activates NF-kappaB.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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LQSHRPAIVRRLHSHVENML--DL-AW---ERGFVSQYECDEIRLPIFTPSQRARRLLDL 187
                             IKDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCEKVE-----QDAARGIIHM 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---QLEEVEFVKPHVVIDGDWYASDED 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLAISCNP--HLNSLNLVKNDFSTSGMLKLCSAFQCPVSNLGIIGLWKQEYY---ARVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAFFGKNPLKNFQQLNLAGNRVSSDGWLAFMGVFE-NLKQLVFFDFSTKEFLPDPALVRK 986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TEGVQQLCQFLRNPECALQRLILNHCNIVDDAYGFLAMRLANNTKLTHLSLTMNPVGDGA
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                                                              Conservative
                                                          4.4%; Score 234.5; DB 4; 20.1%; Pred. No. 3.2e-07; tive 157; Mismatches 384;
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                                                                                          Length 1040;
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RNDTILEV-----W---LRGNTFS----LEEVD---KLGCRDTRL
                                                                                                                                                                                                                    ALHCEQLQKLA-----LFNNKLTDGCAHSMAKLLACRQNFLALRLGNNYITAAGAQVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LALEG-----VFSHKFDFELQDVSSVNEDVLLTTGLLCKYTAQRFKRKKFFHKSFQEY 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QELLLQEGGSPKTTTDMY-----LLILQHFLLHATPPDSASQGLGPSLLRGRLPTLLHLGR 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TEDGEDEEKERETDRERHCSPTDPTSVQTLLENLLQGNLLKNARKVVTSRPAAVSAELRK 436
                                  RMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRL
                                                                                                          L---EEIQLVSCCLSAN-----AVKILAQNLHNLVKLSILDLSENYLEKDGNEALHELID 873
                                                                                                                                              EGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSLRWLSLVGNN----IGSVGAQALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSVEATRAVMKHLAAVYQHGCLLGLSTAKRPLWRQESLQSVKNTTEQEILKAININSFV 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIRTEFNIKGFSEQGIELYLRKRHHEPGVADRLIRLIQETSALHGICHLPVFSWMVSKCH 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGALTAEVGDMTEDSAQALIREVLIKE-LAEGLLLQIQKSRCLRNLMKTPLF--VVITCA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEFLFVFPFSCRQLQCMAKPLSVRTLLFEHCCWP-----DVGQEDIFQLLLDHPDRVLL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKFKFVFFLRLSRAQ------GGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEPVLWRKDQHHHRVEQLTLNGLLQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKAL 194
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                                                                        LMLAKNVMLEELCLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALE
                                                                                                                                                                                ERHITSVTNLKTLSIHDLQNQRLPGGLTDSLGNL----KNLTKLIMDNIKMNEEDAIKLA 784
                                                                                                                                                                                                                                                                                          ---DYNSVGDIGVE-----QLLPCLGV------CKALYLRDNNISDRGICKLIEC
                                                                                                                                                                                                                                                                                                                          NKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCKNIY----SLMVEASPLTIED
                                                                                                                                                                                                                                                                                                                                                                  RSLYEMQEERLARKAARGLNVGHLKLTFCSVGPTECAALAFVLQHLRRPVALQL-----
                                                                                                                                                                                                                                                                                                                                                                                                  FYGGAMASWEKAAEDTGGIHMEEAPETYI---PSRAVSLFFNWKQEFRTLEVTLRDFSKL 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ECGIHLYQESTSKSALSQEFEAFFQGKSLYINSGNIPDYLFDFFEHLPNCASALDFIKLD 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LALWGLGMCCYVFSAQ----QLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCF 609
                                                                                                                                                                                                                                                                                                                                                                                                                                          -CARWCLARSLRKHFHSIPPAAPGEAKSVHAMPG------FIWLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQMGESEFHSHTQTTLFHTFYDLLIQKNKHKH------KGVAAS---DFIRSLDHCGD 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LVVGEAGSGKSTLLQRLHLLWAAG--QDF 322
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RESULT 10 Q9HAV8 ID Q9HAV8 AC Q9HAV8

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF298548; AAG15254.1; -. InterPro; IPR000767; Disease_resist. InterPro; IPR011; LRR. InterPro; IPR011; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00364; DISEASERSIST SMART; SM00370; LRR; 5. SMART; SM00368; LRR_RI; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003592; LRR_out.
InterPro; IPR003590; LRR_RNinh.
Pfam; PF00560; LRR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The PYRIN Domain: A Proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASPASE RECRUITMENT DOMAIN PROTEIN 7. Homo sapiens (Human). Eukaryota, Metazoa; Chordata; Craniat Mammalia; Eutheria; Primates; Catarrh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BERTIN J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYFSCRELAQSKVVSLAELIGKDG-----TATPAPIRQ-----ILSRPERLLFI
 FCIKESRHVK--
                            YLFDFFEHLPNCASALDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSRAVSLF-
                                                         GRNLMQWVPSLQLLLQPHSLESLHCLYETRNKTFLTQVM-AHFEEMGMCVETDMELLVCT
                                                                                           AININSFVEC ----
                                                                                                                                         LLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAK--RPLWRQESLQSVKNTTEQEILK
                                                                                                                                                                                    HP----IPLSYSFIHLCFQEFFAA--MSYVL-----EDEKGRG----
                                                                                                                                                                                                               YTAQREKPKYKFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSS
                                                                                                                                                                                                                                              YLAQALQAQPLGPQLRDLC-SLAAEGIWQKKTLFSPDDLRKHGLDGAIISTFLKMGILQE
                                                                                                                                                                                                                                                                                                                                                                       ALLGSLLGKTILPEASFLITARTTALQNLI--PSLEQARWVEVLGFSE--SSRKEYFYRY 493
                                                                                                                                                                                                                                                                                                                                                                                         ALIREVLIKE-LAEGLLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDGYNEFKPQNCPEIEALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CKALTKEKEVEELRLSRAQGGLEETLCDQLLDIPGTIRKQTEMAMLLKLRQRVLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EENRGHLIEIRDLFGPGLDTQEPRIVILQGAAGIGKSTLARQVKEAWGRGQLYGDRFQHV
                                                                                                                         -KHSNCIIDLEKT----
                                                                                                                                                                                                                                                                                                          FTDERQAIRAFRLYKSNKELWALCLYPWVSWLACTCLMQQMKRKEKLTLTSKTTTTLCLH
                                                                                                                                                                                                                                                                                                                                                                                                                                  LDGVDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISTEFANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRR_RI; 5.
AA; 160880 MW;
                                                                                                                                                                                                                                                                            -----DHCGDLALEGVFSHKFDFELQDVSSVNED-----VLLTTGLLCK 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.18; 20.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0:0-0(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.S.;
                                                                       ----GIHLYQESTSKSALSQEFEAFFQGKSLYINSGN---IPD
                                                                                                                      -LEAYGIHG-LFGASTTRFLLGLLSDEGEREMENIFHCRLSQ
-KLQLIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Mismatches 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 217; DB 4;
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                  --PGWVLQEPSSELCLHWSQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90F809AB838EB7F7 CRC64;
                                                                                                                                                                                                                                                                                                                                          ---LLIQKNKHKHKGVAASDFIRSL---
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 RQHRSTWSPSMVV-LFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Inflammation
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RESULT QUETTA
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Best Local Similarity
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Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL117470; CAB55945.1; -
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
NON_TER 1
SEQUENCE 1192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR003592; LRR_out.
Pfam; PF00560; LRR; 2
PRINTS; PR00364; DISEASERSIST
SMART; SM00370; LRR; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 KDQHHHRVEQLTLNGLLQALQSP--CIIEGESGKGKSTLLQRIAMLWGSGK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----CKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFL 246
                                                                                                                                                                                                                                                                                                                                                                                             FYFSCRELAQSKVVSLAELIGKDG-----TATPAPIRQ-----ILSRPERLLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EENRGHLIEIRDLFGPGLDTQEPRIVILQGAAGIGKSTLARQVKEAWGRGQLYGDRFQHV
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                                                                                ALLGSLLGKTILPEASFLITARTTALQNLI--PSLEQARWVEVLGFSE--SSRKEYFYRY
                                                                                                                                                    ALIREVLIKE-LAEGLLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHT
                                                                                                                                                                                                                                     LDGVDE-
                                                                                                                                                                                                                                                                                                             LDGYNEFKPQNCPEIEALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQ 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human).
stazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AEDCKDLAFGLRANQTLTELDLSFNVLMDAGAKHLCQRLRQPSCKLQRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134610 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 212; DB
Pred. No. 1.3e
97; Mismatches
                                                                                                                                                                                                                                     -PGWVLQEPSSELCLHWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D28D00457C36229A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; 1
1.3e-05;
hes 290;
        LLIQKNKHKHKGVAASDFIRSL---
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MARTINON F., HOFMANN K., Tschopp J.;
MALP1 a novel NACHT, LRR and PYD containing protein.";
"NALP1 a novel NACHT, the EMBL/GenBank/DDBJ databases
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                       MEDLINE-99246063; PubMed-10231032;
Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Somura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
The complete sequences of 100 new cDNA clones from brain which co
                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KIAA0926 PROTEIN (NALP1) (NAC-ALPHA SPLICE VARIANT)
KIAA0926 OR NAC.
                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                        TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRLTD---TEIRIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLAQALQAQPLGPQLRDLC-SLAAEGIWQKKTLFSPDDLRKHGLDGAIISTFLKMGILQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTAQREKPKYKEFHKSEQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSS
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                                                                                                           6:63-70(1999).
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                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                      Homo.
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Best Local Similarity 20.8%;
Matches 184; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2000) to the EMBL/GenBa
EMBL; AB023143; BAA76770.1; -.
EMBL; AF310105; AAG30288.1; -.
EMBL; AF229059; AAK00748.1; -.
InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
Pfam; PF00560; LRR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00364; DISEASERSIST SMART; SM00370; LRR; 5. SEQUENCE 1429 AA; 160944 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Chu Z.-T., Pio F., Xie Z., Godzik A., Reed J.C.,

"NAC: an Apaf-1/Ced-4 family member regulates the
for apoptosis.";
   851
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                           TKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHLSDIGEGMDYIVKSLSSEPCDLEEI
                                                                                    VLSTCKNIYSLMVEASPLTIEDERHITSVTNLKTLSIHDLQNQRLPG-GLTDSLGNLKNL
                                                                                                                                                                                                  YLFDFFEHLPNCASALDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSRAVSLF-
                                                                                                                                                                                                                                                             AININSEVEC ----
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                                                                                                                 WVPVTDAYWQILFSVLKVT-RNLKELD-----
                                                                                                                                                                                                                                                                                         -KHSNCIIDLEKT-----LEAYGIHG-LFGASTTRFLLGLLSDEGEREMENIFHCRLSQ
                                                                                                                                                                                                                                                                                                                     LLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAK - - RPLWRQESLQSVKNTTEQEILK
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                                                                                                                                              -----FNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSL
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AEDCKDLAFGLRANQTLTELDLSFNVLTDAGAKHLCQRLRQPSCKLQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PGWVLQEPSSELCLHWSQ-----
                                                                                                                                                                                                                                                -----GIHLYQESTSKSALSQEFEAFFQGKSLYINSGN---IPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                     -DHCGDLALEGVFSHKFDFELQDVSSVNED-----VLLTTGLLCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 212; DB 4;
Pred. No. 1.7e-05;
7; Mismatches 290
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                                                         LETLRLAGCGLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chu Z.-L., Pio F., Xie Z., Godzik A., "NAC: an Apaf-1/Ced-4 family member re for apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Chu Z.-L., Pio F.,
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID=9606;
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                                                                                AININSFYEC------GIHLYQESTSKSALSQEFEAFFQGKSLYINSGN---IPD
                                                                                                                                                                                                                                                                                                                                                                                     YLAQALQAQPLGPQLRDLC-SLAAEGIWQKKTLFSPDDLRKHGLDGAIISTFLKMGILQE
                                                      GRNLMQWVPSLQLLLQPHSLESLHCLYETRNKTFLTQVM-AHFEEMGMCVETDMELLVCT
                                                                                                                                                             -KHSNCIIDLEKT-----LEAYGIHG-LFGASTTRFLLGLLSDEGEREMENIFHCRLSQ
                                                                                                                                                                                                                    LLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAK--RPLWRQESLQSVKNTTEQEILK
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Pred. No. 1.8e-05;
77; Mismatches 290
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Q9BZZ9;
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Mammalia; Eutheria;
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                                                                             FTDERQAIRAFRLVKSNKELWALCLVPWVSWLACTCLMQQMKRKEKLTLTSKTTTTLCLH
                                                                                                                                                                               ALLGSLLGKTILPEASFLITARTTALQNLI--PSLEQARWVEVLGFSE--SSRKEYFYRY
                                                                                                                                                                                                                                  ALIREVLIKE-LAEGLLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHT
                                                                                                                                                                                                                                                                                       LDGVDE----
                                                                                                                                                                                                                                                                                                                                    LDGYNEFKPONCPEIEALIKENHRFKNMVIVTTTTECLRHIROFGALTAEVGDMTEDSAO
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                                                                                                                                  FYD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GLRH--PACKLIRLGLDQTTLSDEMRQELRAL
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Primates;
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-DHCGDLALEGVFSHKFDFELQDVSSVNED-----VLLTTGLLCK
                                                                                                                                                                                                                                                                                       -----PGWVLQEPSSELCLHWSQ------PQPAD
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 207.5; DB 4; Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                             -LLIQKNKHKHKGVAASDFIRSL---
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Best Local Similarity
Matches 173; Conserv
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Q9BZZ8;
                                                                                                                                                                                                                                                                                                             Chu Z.-L., Pio F., Xie Z., Godzik A., Reed J.C.;
"NAC: an Apaf-1/Ced-4 family member regulates the cytochrome for apoptosis.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF229062; AAK00751.1;
SEQUENCE 1443 AA; 162237 MW; C30E9BE9EC82FE96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NAC-DELTA SPLICE VARIANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
 409
                                  247
                                                                                                                                                                            142 KDQHHHRVEQLTLNGLLQALQSP--CIIEGESGKGKSTLLQRIAMLWGSGK-----
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                                                                     365 FYFSCRELAQSKVVSLAELIGKDG-----TATPAPIRQ-----ILSRPERLLFI 408
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LDGVDE------PGWVLQEPSSELCLHWSQ------
                                 LDGYNEFKPQNCPEIEALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQ 306
                                                                                                          ----CKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFL
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                                                                                                                                             EENRGHLIEIRDLFGPGLDTQEPRIVILQGAAGIGKSTLARQVKEAWGRGQLYGDRFQHV 364
                                                                                                                                                                                                                     3.9%; Score 207.5; DB 4; Length 1443; llarity 21.0%; Pred. No. 3.4e-05; Conservative 91; Mismatches 280; Indels 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Primates;
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QLVSCGLTSDCCQDLASVLSASPSLKELDLQQNNLDDVGVRLLCE
                                QLVSCCLSANAVKILAQNIHNLVKLSILDLSENYLEKDGNEALHE 870
                                                                                                           TKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHLSDIGEGMDYIVKSLSSEPCDLEEI 825
                                                                                                                                               VKSLCK-----TLRRPRCL------LETLRLAGCGLT-----
                                                                                                                                                                                  VLSTCKNIYSLMVEASPLTIEDERHITSVTNLKTLSIHDLQNQRLPG-GLTDSLGNLKNL
                                                                                                                                                                                                                        WVPVTDAYWQILFSVLKVT-RNLKELD----------------LSGNSLSHSA
                                                                                                                                                                                                                                                        ----FNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSL
                                                                                                                                                                                                                                                                                               FCIKFSRHVK-----KLQLIEG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLAQALQAQPLGPQLRDLC.SLAAEGIWQKKTLFSPDDLRKHGLDGAIISTFLKMGILQE
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## ALIGNMENTS

C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000

neuronal apoptosis inhibitory protein 2 - mouse

C; Accession: T42628

T42628

Š DЪ δÃ 멍 δÃ DЬ Qy DЪ Qy DЬ Qy Qy A;Cross-references: EMBL:AF102871; NID:g3860228; PID:g3860229; PIDN:AAC73002.1 C;Genetics: A;Gene: Naip2 R:Yaraghi, Z: Diez, E: Gros, P: MacKenzie, A. Mamm. Genome 10, 761-763, 1999
A:Title: CDNA cloning and the 5'genomic organization A:Reference number: Z22179; MUID:99315342
A:Accession: T42628
A:Status: preliminary; translated from GB/EMBL/DDBJ В Вb A; Molecule type: mRNA A; Residues: 1-1447 < YAR> Query Match Best Local Matches 268; 433 719 663 322 809 551 494 146 445 404 206 38 VNIICCEKVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGD 97 QRFKPKYKFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSSLLR 492 SLKHKG-AAKPLQATVSSCGQLALTGLFSSCFEFNSDNLAEAGVDEDEELTTCLMSKFTA KHKHKGVAASDFIRSLDHCGDLALEGVFSHKFDFELQDV--SSVNEDVLLTTGLLCKYTA 432 HTLITKNYLSRTCLLIAVHTNKVRGIRPYLDTSLEIKEFPFYNTVSVLRKLFSHD-----HHRVEQUTLNGLLQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRL 205 LDDLAQDLKDLYHTPSFLNF------YPLGEDIDIIFNLKSTFTEPVLWRKDQH 145 LLQIQK -----SRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKN EALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKELAEGL 321 ---QGSLTIPEVFSNLNSVMCVEGEAGSGKTTFLKRIAFLWASGCCPLLNRFQLVFYLSL 550 -RSLSEQLRDTYTKATFRHMNLPEVYSSLGTDHLLSCDVSII---SKHISQPV------ 493 VSVLCRDQ-DHSEAQG-----RGCASSGTYLPS-----TDL-GQSEAQWLQEA- 444 IMRVRKFINYFGFHEELQGIHKTPLFVAAVCTDWFKNPSDQPFQDVALFKAYMQYL----Similarity 12.0%; Score 632.5; DB 2; ilarity 24.2%; Pred. No. 3.1e-29; Conservative 195; Mismatches 423; of Naip2, Length 1447; Indels 221; candidate Gaps 662 44;

F;618,632,823,923,1035/Binding site: carbohydrate (Asn) (covalent) #status

predicted

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A; Molecule type: mRNA
A; Residues: 1-123 < ROY>
A; Residues: 1-123 < ROY>
A; Cross-references: GB:U19251
C; Genetics:
A; Gene: GDB:SMA@; SMA
A; Cross-references: GDB:120378; OMIM:600354; OMIM:253300
A; Map position: 5q12.2-5q13
C; Keywords: apoptosis; ATP; glycoprotein; nucleotide binding; P-1
F; 94-110/Domain: transmembrane #status predicted <TMM1>
F; 470-477/Region: nucleotide-binding motif A (P-10op)
F; 470-496/Domain: transmembrane #status predicted <TMM2>
F; 476/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                               neuronal apoptosis inhibitory protein - human N; Alternate names: NAIP C; Species: Homo sapiens (man) C; Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001 C; Accession: A55478 R; Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, d. T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A. Cell 80, 167-178, 1995 A; Title: The gene for neuronal apoptosis inhibitory protein is partially delapse for neuronal apoptosis inhibitory protein is partially delapse.
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                           SEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSIL
                                                          FPNFHHMEKLLIQISAEYDPSKLVASLPNFISLKILNLEGQQFPDEETSEKFAYILGSLS
                                                                                                                      AAEQELLLTLPSLESLEVSGTTQSQDQIFPN--LDKFLCLKELSVDLEGNINVFSVIPEE
                                                                                                                                                    IEDERHITSVTNLKTLSIH---DLQNQRLPGGLTDSLGNLKNLTKLIMDNIKM-----
                                                                                                                                                                                     NDIDVVGQDMLEILMTVFSASQRIELHLNHSRGFIESIRPALELSKASVTKCSISKLELS
                                                                                                                                                                                                                RDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLSTCK-NIYSLMVEASPLT
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NLEELILPTGDGIYRVAKLIIQQCQQLHCLRVL 1217
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A:Molecule type: mRNA
A:Residues: 1-1192 <KOE>
A:Cross-references: EMBL:AL117470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-C;Accession: T17255
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18722
A;Accession: T17255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: DKFZp58601822.1
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Hest Local Similarity 20.8%;
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                                                                                            VLSTCKNIYSLMVEASPLTIEDERHITSVTNLKTLSIHDLQNQRLPG-GLTDSLGNLKNL 765
                                                                                                                                             WVPVTDAYWQILFSVLKVT-RNLKELD-
                                                                                                                                                                      -----FNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSL
                                                                                                                                                                                                                                                                                           GRNLMQWVPSLQLLLQPHSLESLHCLYETRNKTFLTQVM-AHFEEMGMCVETDMELLVCT
                                                                                                                                                                                                                                                                                                                             AININSFVEC ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTAQRFKPKYKFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLAQALQAQPLGPQLRDLC-SLAAEGIWQKKTLFSPDDLRKHGLDGAIISTFLKMGILQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTDERQAIRAFRLVKSNKELWALCLVPWVSWLACTCLMQQMKRKEKLTLTSKTTTLCLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYFSCRELAQSKVVSLAELIGKDG-----TATPAPIRQ-----ILSRPERLLFI
                                                                                                                                                                                                                                                     YLFDFFEHLPNCASALDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSRAVSLF-
                                                                                                                                                                                                                                                                                                                                                               -KHSNCIIDLEKT-----LEAYGIHG-LFGASTTRFLLGLLSDEGEREMENIFHCRLSQ
                                                                                                                                                                                                                                                                                                                                                                                                  LLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAK--RPLWRQESLQSVKNTTEQEILK 547
                                                                                                                                                                                                                                                                                                                                                                                                                                    HP---IPLSYSFIHLCFQEFFAA--MSYVL-----EDEKGRG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLGSLLGKTILPEASFLITARTTALQNLI--PSLEQARWVEVLGFSE--SSRKEYFYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIREVLIKE-LAEGLLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDGYNEFKPQNCPEIEALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
-- AEDCKDLAFGLRANQTLTELDLSFNVLTDAGAKHLCQRLRQPSCKLQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DHCGDLALEGVFSHKFDFELQDVSSVNED-----VLLTTGLLCK 429
                                                                       -TLRRPRCL-
                                                                                                                                                                                                                                                                                                                           ---GIHLYQESTSKSALSQEFEAFFQGKSLYINSGN---IPD
                                                                                                                                                                                                                     KLQLIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97;
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Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -PGWVLQEPSSELCLHWSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human (fragment)
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                                                                       -LETLRLAGCGLT--
                                                                                                                                             -----LSGNSLSHSA
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                                                                                                                                                                                                                   -RQHRSTWSPTMVV-LFR
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protein T7N9.24 [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (c.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C.Accession: B86398 R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Chin, C.W.; Chung, M.K.; J. Johnson-Hopson, C.; Khan, S.; Khaykin, Nature 408, 816-820, 2000 A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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A; Map position: 1
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A; Residues: 1-1590 <STO>
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A;Accession: B86398
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PPTQGLLELSKKIAEVTGLLPLAVKVFGSH-----FYDKDENEWQVELEKLKTQQDK
                                            -----LMKTPLEVVITCAIQMGESEFHSHTQTTLFHTFYDL------LIQKNKHK 377
                                                                                                                                               MLLKLRQRVLFLLDGYNEFKPQNCPEIEAL-----IKENHRFKNMVIVTTTTECLRHIR 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WCLDELALLCDLRSSLKRPMIPIFYGVNPEDVRKQSGEFRKDFEEKAKSFDEETIQRWKR 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQNVRVFRDNEGMEKGDKIDPSLF-------EAIEDSAASVIILSTNYANSS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCEKVEQDAARGIIHMILKKGSE 64
                                                                                                QVNALVGETSWYGEGSLIVITTRDSEILSKLSVNQQYEVKCLTEPQALKLFSFYSLRKEK
                                                                                                                                                                                                                                                                                                                                                  LQRIAMLWGSGKCKALTKFKFVFFLR----LSRAQGGLFETLCDQLLDIPGTIRKQTFMA 234
                                                                                                                                                                                                                                                                                                                                                                                                         SPIKDLMKLFNTESS - - ·
                                                                                                                                                                                                                                                                                                                                                                                                                                      ---EDIDIIFNLKSTFTEPVLWRKDQHHHRVEQLTLNGLLQALQSPCIIEGESGKGKSTL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMNLVGNIPGYVCTAKTVGDDNEGINREKVDDMIDLVVKKVVAAVRNRPEIVADYTVGLE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SC--NLFL-----KSLKEWNYPLFQDLNGQSLFHQTSE--GDLDDLAQ-----
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                                                                                                                                                                                                                                                                                                    -----AKAFYNKIIVNFNRHRVFIESVRGKSSDQ--DGLVNLQKTLIKELFRL 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.8%; Score 198.5; DB
20.5%; Pred. No. 0.0014;
tive 160; Mismatches 42
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                                                                                                                                                                                                ----PEIEDVSIGLEKIKENVHEKKIIVVLDDVD---HID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DLKDLY------HTPSFLNFYPLG-- 121
                                                                                                                                                                                                                                                                                                                                                                                                    -SGIQVMGLY------GMGGIGKTTL 434
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J
B
A: Reference number: Z15359
A: Accession: T04426
A: Molecule type: DNA
A: Residues: 1-1405 <BEV>
A: Cross-references: EMBL: AL021687
A: Experimental source: cultivar Columbia; BAC clone T18B16
R: Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, submitted to the Protein Sequence Database, February 1998
A: Reference number: Z15395
A: Accession: T05042
A: Molecule type: DNA
                                                                                                                                                                         RESULT 5

T04426

T04426

N;Alternate names: hypothetical protein F13C5.220

N;Alternate names: hypothetical protein F13C5.220

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999

C;Accession: T04426; T05042

R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansorge, W.; Bancroft, I.

submitted to the Protein Sequence Database, April 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INNVELEGD-LKLLP---SELKWIQ------WK-----GFPLENLPPDILSRQL
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                                                                                                                                                                                                                                                                                                                                                                                                                            RLPKSFGDLKSLHRLYMQETLVAELPESFGNLSNLMVLEMLKKPLFRISESNVPGTSEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILGAFFG--KNPLKNFQQLNLAGNRVSSDGWLAFMGVFENLKQLVF--FDFSTKEFLPDP 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLRNCKSLKALPKTIGKMDTLYSLNLVGSNIEELPEEFGKLENLVELRMNNCKM---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVLDLSESGVRRVKTLPRKRGDENLKVVNLRGCHGLEAIPDLSNHNA-----LEKLVLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AVSLFFNWKQEFRTLE------VTLR-----DFSKLNKQDITYLGKIFSSA 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GIYSVFNYLKNKLVR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WRQESLQSVKNTTEQEILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSLYINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGNGYLQKMVSISDITSTYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPL 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KMDITKEEVVDILKGCGLNAEAA 677
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                                                                   H.W.;
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                       ELPDKISELSNLKELII-
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A;Residues: 1-1405 <BEW>
A;Cross references: EMBL;AL021711
A;Experimental source: cultivar Columbia; BAC clone F13C5
C;Genetics:
C;Genetics: 4
A;Map position: 4
A;Map position: 4
A;Introns: 893/3; 1164/2; 1183/3; 1192/3; 1198/2; 1214/3; 1251/1; 1282/2; 1327/1;
A;Note: T18B16.20; F13C5.220
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                              VKLSILDLSENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVP 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKIFKELILSSKSLDEAAASKNAIDRSRYNPVLQLSYELLKPDETVKRPVIAC--FWHIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-----HCGDL----ALEGVFS--HKFDFELQDVSSVNEDVLLTTGLLCKYTAQRFK
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                                                                                                                                                       KNLKKMCLFHLTHLSDIGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNL
                                                                                                                                                                                                                                                                  TNL-----KTLSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEGL
                                                                                                                                                                                                                                                                                                                       ETKIIRLPIFHLKDSTNDFSTMPILTRLLLRNCTRLKRL-PQLRPLTNLQILDACGATDL
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                                                                                                                                                                                                               VEMLEVCLEEKKELRILDMSKTSLP-ELADTIADVVNLNKLLLRNCSLIEE------L
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -FENWKQEFRTLEVTLRDFSKLNKQDITYLGKIFS
                                                                                                                                                                                                                                                                                                                                                                       --LVLSTCKNIYSLMVEASPLT---IEDERHITSV
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                                                                                                     EVFDVSGCIK---LKNINGSFGEM
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C;Accession: G96663
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
Rauthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia A.; Li, Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719
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G96663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AE005173; NID: g6358786; PIDN: AAF07367.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA A; Residues: 1-1031 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T12P18.11 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Best Local Similarity
Matches 206; Conserv
     498
                                                                                                                                                         378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211 VKMV-----GISGPAGIGKTTIARAL------QSRLSNKFQLTCFV------DNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 IEKIARDVSDKLNATPS-----RDFNGMVGLEAHLTE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 NETCAHRTDEDKON------WSKALKD-----VGNIAGEDFLRWDNEAKM 167
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SVEA----TRAVMKHLAAVYQHGCLLGLS----IAKRPLWRQESLQSVKNTTEQEILKAI 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETL 216
: | | : | : | : | : | : |
                                                                                                 YKFFHKSFQEYTAGRRLSSLLTSHEPEEVTK-GNGYLQKMVSISDITSTYSSLLRYTCGS 497
                                                                                                                                                                                                KGVAASDFIRSLDHCGDLALEGVFSHKFDFELQDVSSVNEDVLLTTGLLCKYTAQRFKPK 438
                                                                                                                                                                                                                                                                                                    EGLLLQIQKSRCLRNLMKTPLFVVITCAIQMGESEFHSHTQTTLFHTFYDLLIQKNKHKH 378
                                                                                                                                                                                                                                                                                                                                                       QLEALANETTWFGSGSRIVVTTENKEILQQHGINDLYHVGFPSDEQA----FEILCR---
                                                                                                                                                                                                                                                                                                                                                                                                   EIEALIKENHRFKNMVIVTTTTECLRHIRQFGALTA-EVGDMTEDSAQALIREVLIKELA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESFLNSLDELRLQEQFLAKVLNHDGIRICHSGVIEERLCKQRVLIILDDVNHIM----- 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDQLLDIPGTIR-KQTFMAMLLK------LRQRVLFLLDGYNEFKPQNCP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDDLAQDLKD-LYHTPSFLNFYPLGEDIDIIFNLKSTFTEPVLWRKDQHHHRVEQLTLNG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIICCEKVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGD- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVFENLKQLVFFDFSTKEFLPDPALVRKLSQVLSKLTFL 997
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                                               -EEWEEVI--RRLETILDHQDIEEVLRVGYGSLHE--NEQSLFLHIAVFFNYTDGD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 167; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.4%; Score 178.5; DB 2; 19.2%; Pred. No. 0.011;
                                                                                                                                                                                                                                                     ----YAFRKTTLSHGFEKLARRVTK---
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                                                                                                                                                   -GLRVLGSSLRGKNE
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TEHLEVEIIHPHLPEIDPSEVSREIV-FEESSKENHEDVIDCGAKFLTDGSI 984		934	Ъ
QLNLAGNRVSSDGWLAFWGVFENLKQLVFFDFSTKEFLPDPAL 983		941	Ωу
RPGTGFVVCIVISPNLASQITEY-RLPQLLCRRRIGQGDLDPIEKVFNVRTLLNFQ 933		879	Db
SLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPLKNFQ 940	1	895	Qy
GQQAQRAIVQRSLLLGTTLLPGRELPAEFDHQGKGNTLTI 878	NCFKL	834	DЬ
NLVKLSILDLSENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQG 894	NLVKLSILDI	846	ОУ
SLHLLYILNISGCRRLASLPE-LPSSLRFLMADDCESLETVFCPLNTPKAELNFT 833		780	DЪ
NLKKMCLFHLTHLSDIGEGMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLH 845		789	Qy
LYVSRTAVEGMPPSIRFCSRLERLSISSSGKLKGITHLPISLKQLDLIDSDIETIPECIK 779		720	Db
NORLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAEGLK 788		748	Qy
LVEIPSSFSHLHKLEWLEMNNCINLQVIPAHMNLASLETVNMRGCSRLRNIPVMSTNITQ 719		660	рь
VAGSLSLVLSTCKNIYSLMVEASPETIEDERHITSVTNLKTLSIHDLQ 747		700	QΥ
PQYLVELYMPSSQLEKLWEGTQRLTHLKKMNLFASRHLKELPDLSNATNLERMDLSYCES 659		600	
PSRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSL-RLQIKRCAG 699		645	Qy
-LRFLKVFKSRDDGNDRVHIPEETEFPRRLRLHWEAYPCKSLPPTFQ 599	;	553	ф
CASALDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYI 644		605	Qy
LIHAPEICDVLEYATGTKAMSGISFDISGVDEVVISGKSFKRIPN 552		508	DЪ
NINSFVECGIHLYQEST-SKSALSQEFEAFFQGKSLYINSGNIPDYLFDFFEHLPN 604		550	Qy
LVKAMFTDNNLDIKHGLKILADKSLINISNNREIVIHKLLQQFGRQAVHKEEPWKHKI 507		450	Db

ABDOAN
alpha-actinin - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 22-Jun-1999
C;Accession: \$00103; A29006
R;Noegel, A.; Witke, W.; Schleicher, M.
FBS Lett. 221, 391-396, 1987
A;Title: Calcium-sensitive non-muscle alpha-actinin contains EF-hand structures and h A;Reference number: \$00103; MUID:87304850
A;Reference number: \$00103; MUID:87304850
A;Residues: 1-862 < NOED
A;Cross-references: EMBL:Y00689; NID:g7177; PIDN:CAA68685.1; PID:g7178
A;Cross-references: EMBL:Y00689; NID:g7177; PIDN:CAA68685.1; PID:g7178
A;Cross-references: EMBL:Y00689; NID:g7177; PIDN:CAA68685.1; PID:g7178
A;Cross-references: EMBL:Y00689; NID:g7177; PIDN:CAA68685.1; PID:g7207
A;Cross-references: EMBL:Y00689; NID:g7177; PIDN:CAA68685.1; PID:g7207
A;Cross-references: EMBL:Y00689; NID:g7207; PIDN:CAA68685.1; PID:g72034
A;Cross-references: EMBL:X04324; NID:g7202; PIDN:CAA27855.1; PID:g929034
A;Cross-references: EMBL:X04324; NID:g7202; PIDN:CAA27855.1; PID:g929034
A;Cross-references: EMBL:X04324; NID:g7202; PIDN:CAA27855.1; PID:g929034
C;Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology: calmodulin
C;Keywords: actini binding; calcium binding; duplication; EF hand; homology: calmodulin
C;Keywords: actini binding; calcium binding; duplication; EF hand; homology: calmodulin
C;Keywords: actini binding; calcium binding; duplication; EF hand; homology: calmodulin
C;Keywords: actini actin-binding domain homology <cry>F;506-07/Domain: spectrin/dystrophin repeat homology <cry>F;506-07/Domain: spectrin/dystrophin repeat homology <cry>F;706-798/Domain: calmodulin repeat homology<cry>F;706-798/Domain: calmodulin repeat homology<cry>F;706-798/Domain: calmodulin repeat homology<cry>F;706-798/Domain: calmodulin repeat homology

Gaps

61;

97

76

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RESULT 8
T06146
disease resistance protein homolog F24J7.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06146
R;Bevan, M; Vitale, D; Liguori, R; Argiriou, A; De Simone, V.; Bancroft
submitted to the Protein Sequence Database, April 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSLYINSGNIPDYLFDFFEHLP
                                                                                                                                                                                                                           DPALVRKLSQVLSKLTFLQEARLVGWQFDD------DDLSVITGAFKLV 1022
                                                                                                                                                                                                                                                                                                                                                                        LEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRELGRSENDYSVISYDELSAKWNNLLAGIEERKVQLANELTTQTNNDVLCQSFSVKANE
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                                                                                                                                                                                                                                                                                                TDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFMGVFENLKQLVFFDFSTKEFLP
                                                                                                                                                                                                                                                                                                                                    TIRSQLEEA-QVVDNKHTQHSLESLKLKW-----DKLNTLAKKNEQVVEGEILAKQLTGV
                                                                                                                                                                                                                                                                                                                                                                                                             ISDYVRVTLDAISQNTSSDP--QEQLNNIRAIITAHAEK-------KPELDELY
                                                                                                                                                                                                                                                                                                                                                                                                                                              IGE----GMDYIVKSLSSEPCDLEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSENY 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGNL----KNLTKLIMDNI--KMN-----EEDAIKLAEGL---KNLKKMCLFHLTHLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NVWIEAADDHVFDPINVDSVQGVQEIQEKFDAFLHD-QSQQFAELEALAALTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FAQQWTGVKSSAETYKNTLLAELERLQKIEDSLVEF---AKRAAQL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLFFNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N------LEAFDGECQSLEGQSNSDLLSILAQLTELNYNGVPELTERKDTF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSLLTSHEPEEVTKGNGYLQKMVSISD-ITSTYSSLLRYTCGSSVEATRAVM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAFDIAEKELDIPKMLDVSDMLDVVRPDERSVMTYVAQ----YYHHFSASRKAETAGKQV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LE-GVFSHKFDF-ELQDVSSVNEDVLLTTGLLCKYTAQRFKPKYKFFHKSFQEYTAGRRL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----KTEGYDRVKVGNFHTSFQDGLAFCALIHKHRPDLINFDSLNKDDKAGNLQ
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                                                                                                                                                                                       -QLNQVISKIDTDGNGTISFEEFIDYMVSSRKGTDSVESTKAAFKVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 176; DB 1; Length 862; Pred. No. 0.012;
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                      Mewes,
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A;Accession: T06146
A;Molecule type: DNA
A;Residues: 1-1167 <BEV>
A;Cross references: EMBL:AL021768; GSPDB:GN00062; ATSP:F24J7.90
A;Experimental source: cultivar Columbia; BAC clone F24J7
C:Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                         EILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSLYINSGNIPDYLFDFFEHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLLQALQSPCIIEGES------GKGKSTLLQRIAMLWGSGKCKALTK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---FNSKSKEKETTLIDKIVDAVLQKLSKISSEESTSGSVDQGRGEEVEEAKADKISGLN
                                                                                                                                                                                                                                                                                                                                                                                                                                              YDLLIQKNKHKHKGVAASDFIRSLDHCGDLALEGVFSHKFDFELQDVSSVNEDVLLTTGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRLKELEEKVAITGDKRDETRIVEVVGMPGIGKSTLLKAFYETW----KTRFLSSALLQNI
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                                       QIWREE-----KDAPKLRWVDLNHSSKLENLSGLSQALNLERLNLEGCTALKTLLLG
                                                                                                                                                   ----NCASALDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSRAVSLFFN----
                                                                                                                                                                                                                                                                                                TSTYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWRQESLQSVKNTTEQ
                                                                                                                                                                                                                                                                                                                                    ELGPEARDDDGRGRHRIWHHHNQDNKG--RLNRLL--KRPGGSTSVRSFFLDMYVMKTDV
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                                                                           --WKQEFRTLEVTLRDFSKLNKQDITYLGKI---
                                                                                                                 LEEVRCLHWLNEPK-
                                                                                                                                                                                       -- LRYLKFYS----SHCPQECTPKENI---
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     -LQIKRCAGVAG----
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20.1%;
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%; Pred. No. 0.035;
141; Mismatches 3
     -SL-SLVLSTCKNIYSLMVEASPLTIEDERHITS
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                                                                                                                 -DELPQDFIPKNLVDLKLPYSKIR
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resistance complex protein I2C-1 - tomato (;Species: Lycopersicon esculentum (tomato) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 17-Nov-2000 C;Accession: T06403 R;Ori, N.; Eshed, Y.; Paran, I.; Presting, G.; Aviv, D.; Tanksley, S.; Zamiz Plant Cell 9, 521-532, 1997 A;Title: The I2C family from the wilt disease resistance locus I2 belongs to A;Reference number: Z15652; MUID:97290204 A;Accession: T06403
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Best Local Similarity 19.8
Matches 231; Conservative
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                                                          MLSYNDLPAHLKQ----
                                                                                                                                                                                                                             TPSFLNFYPLG----EDIDIIFNLKSTFTEPVLWRKD-QHHHRVEQL-----TLNGL--
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                                                                                            CDQLLDIPGTIRKQTFMAMLLKLRQRVLFLLDGYNEFKPQNCPEIEALIKENHRF-KNMV
                                                                                                                                  ALKALAGMLRSKSEVDEWRNILRSEI - -
                                                                                                                                                                  -LQALQSPCIIEGESGKGKSTLLQRIAMLWGSGKCKALTKFKFVFFLRLSRAQGGLFETL
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                                                                                                                                                                                                    ------MGILSSEDSWALFKRHS-----LEHKDPKEHPEFEEVGKQIADKCKGLPL
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disease
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protein
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Pred. No. 0.043;
1; Mismatches 393;
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submitted to the EMBL Data Library, A;Description: The sequence of C. el A;Reference number: S69019
A;Accession: T15864
A;Accession: preliminary; translated fi A;Status: preliminary; translated fi A;Molecule type: DNA
A;Residues: 1-1066 <FUL>
                                                                                                                                               hypothetical protein C56E6.6 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-C;Accession: T15864
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572

EMBL: U39996; NID: g1055114; PID: g1055120; PIDN: AAA81094.1;

CESP:C56E6

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probable disease resistance protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84547
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C;Genetics:
A;Gene: CESP:C56E6.6
A;Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, M.; Ko, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venature 402, 761-768, 1999
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                                                                                                                                                                                                                                                                                                                                   DVQGSLSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNE - - EDAIKLAEGLKNLKKMCLFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSSELK-----SLNLAHNKIHSISSRSFSDLDNLQQLRLSHNNIRTITSMTFSNLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHFPSLFRLDKLRHLMLDNNQIQKIDNF--SLADLPKLQHLSLAGNQLDI-ITENMFGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNKIMSLKKPTSLLSITKEETSTVRRLN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KRPLWRQESLQSVKNTTEQEILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDSSFETVGHMQSLDLSYNRIAYLPRGML--KNFAKTLKTLKLAENMIHATPEALRDLRN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITEIQKMSLPQTLKFLYLRNNLLTQIPYVALNDLKTLQSIDLEGNNITHLMDTNEVTFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 114; Mismatches 299;
                                                                                                                                                                                                                          -GAFENLLSLKILDLSNNPVTSWSPTAFRDLSHSISSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LSDIGEGMDYIVKSLSSEPCDLEEIQLV-----SCCLSANAV-KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.2%;
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Pred. No. 0.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---KHSFRSFRKIRELDISYNQIQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                FG----NLSILSFANNKVD
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                                                                                                                                                                                                                                                                                                                                                                                                            ---LEQLTALMLPWGC
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                                      C.Y.;
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813

KSLSSE--

PCDLEEI --

-QLVSCCLSANAVKILAQNLHNLVKLSILDLSE--

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A;Title: Sequence and analysis of chromosome A;Reference number: A84420; MUID:20083487 A;Recession: F84547 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-110 <STO> A;Cross_references: GB:AE002093; NID:96598362
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Best Local Similarity
Matches 187; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGYNEFKPQNCPEIEALIKENHRFKNMVIVTTTTECLRHI-----RQFGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQLTLNGLLQALQS--PCIIEGE------SGKGKSTLLQ------RIAMLWG
                          NLKNLTKLIM---DNIKMNEEDAIKLAEGLKNLKKMCLFHLTHLSDIGEG-----MDYIV
                                                            ILSHCKNFEQFPVISECLEALYLQGTAIKCIPTSIENLQKLILLDLKDCEVLVSLPDCLG
                                                                                      VLSTCKN-----IYSLMVEASPLTIEDERHI-TSVTNLKTLSIHDLQNQRLPGGLTDSLG
                                                                                                                        DISGLIGAHNIRRLNLEGCIELKTLPQEMQEMESLIYLNLGGCTRLVSLPEFKLKSLKTL
                                                                                                                                                                                      LQFPLKKLSKAFNPKNLIELNLPYSKITRLWKES----
                                                                                                                                                                                                                     --IPSRAVSLFFN---
                                                                                                                                                                                                                                                  LKVYN------SQCSRDCDVGCKLTFPDGLKCS------
                                                                                                                                                                                                                                                                                INSGNIPDYLFDFFEHLPNCASALDF-IKLDFYGGAMASWEKAAEDTGGIHMEEAPETY-
                                                                                                                                                                                                                                                                                                                                                                             RDFAGNLL----ISISSGRLEMHDLMATFAKKLCSSLSNENNYGYQMIWNHESFNAAAK
                                                                                                                                                                                                                                                                                                                                                                                                          TSTYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLS----IAKRPLWRQESL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGLLCKYTAQRFKPKYKFFHKSFQEYTAGRRLSSLLTSHEPEEVTKGNGYLQKMVSISDI 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LLIQKNKHKHKGVAASDFIRSLDHCGDLA---LEGVFSHKFDFELQDVSSVNEDVLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VITTRDKISISQFEYTYVVPRLNITDGLKQFSFYAFEDHNCPYPGNLMDLSTKFVDYARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VITCAIQMGESEF-HSHTQTTL-----FHTFYD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LTAEVGDMTEDSAQALIREVLIKELAEGLLLQIQKSRCLRNLM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YDEWK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGKCKALTKFKFVFFLRLSRAQGGLFETLCDQLLDIPGTIRKQTFMAMLLKLRQRVLFLL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQLLINQIVGEVORVIKIISQGEGDEKNKMVCTNTSTGSSFIPQNRNMVDPENQIELVGL 126
 NLRSLQELILSGCSKLKFFPE----LKETMKSIKILLL--
                                                                                                                                                       -LGKIFSSATSLRLQIKRC---
                                                                                                                                                                                                                                                                                                                NKRMRYVNQPRKKVTESEMDNVMGI------LLDVSEMDNNMTLDSKFFSEMCNLRY
                                                                                                                                                                                                                                                                                                                                              -----QSVKNTTEQEILKAININSFVECGIHLYQESTSKSALSQEFEAFFQGKSL-Y
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18.7%;
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                                                                                                                                                       AGVAGSLS-----L
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A;Experimental source: cultivar Cf 2
A;Accession: T10515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1112 <DIX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-1066,'I',1068-1085,'E',1087-1110,'R',1112 <DI2>
A;Cross-references: EMBL:U42445; NID:91184076; PIDN:AAC15780.1;
A;Experimental source: cultivar Cf 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease resistance protein Cf-2.1 - currant tomato
C;Species: Lycopersicon pimpinellifolium (currant tomato)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
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R; Dixon, M.S.; Jones, D.A.; Keddie, J.S.; The Call 84, 451-459, 1996
Title: The tomato Cf-2 disease resistance Reference number: Z17062; MUID:96190812
A; Accession: T10504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 139; Conserv
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                                                                                                                                                                                                                                                                                                                                                  EICYLRSLTYLDLSENALNGSIPASLGNLNNLSFLFLYGNQLSG--SIPEEIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFTWRKSQMMSDALNRYNGGFVLESLVSTCFP-GCEVPAS
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  YLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGSLSSLLKHLEEVPQLVKLGLKNWR 918
                                                                                                                                                       GNLKNLTKLIMDNIKMNEEDAIKLAEGLKNLKKMCLFHLTHLSDIGEGMDYIVK----SL
                                                                                                                                                                                               --GSTPASLGNLKNLSRLNLVNNQLSGSTP---ASLGNLNNLSMLYLYNNQLSGSTPASL
                                                                                                                                                                                                                                 VAGSLSLVLSTCKNIYSLMVEASPLTIEDERHITSVTNLKTLSIHDLQNQRLPGGLTDSL 759
                                                                                                                                                                                                                                                                                                                                                                                        ---YL----FDFFEHLPN---CASALDFIKLDF---YGGAMASWEKAAEDTGGIHMEEA 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STYSSLLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAKRPLWRQESLQSVKNTTEQE 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLLAKLQIIR-----IFHNQ------LNGFIPKEI----GYLRSLTKLS-LG 175
                                        SNNSINGFIPASFGNMSNLAFLFLYENQLASS-----VPEEIGYLRSLNVLDLSEN
                                                                                                                  GNLNNLSMLYLYNNQLSGSIPASLG-NLNNLSRLYLYNNQLSGSIPEEIGYLSSLTYLDL
                                                                                                                                                                                                                                                                                                            PETYIPSRAVSLFFNWKQEFRTLEVTLRDFSKLNKQDITYLGKIFSSATSLRLQIKRCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILKAININSFVECGIHLYQESTSKSALSQEFEA-----FFQGKSLYINSGNIPD 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            -----SDNALNGSIPASLGNMNNLSFLFLYGNQL---SGSIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --IDRMN---VLEQLTALMLPWGCDVQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GSIPASVGNLNNLSFLYLYNNQLSGSI - - - - - PEEISYLRSLTELD
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                                                                                                                                                                                                                                                                       -----RSLNVLGLSENALN----
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21.6%; Pred. No. 0.08;
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                                                                            -LEEIQLVSCCLSANAVKILAQNLHNLVKLSILDLSEN
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A;Accession: T06145
A;Molecule type: DNA
A;Residues: 1-1715 <BEV>
A;Cross-references: EMBL:AL021768; GSPDB:GN00062; ATSP:F24J7
A;Experimental source: cultivar Columbia; BAC clone F24J7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #tex
C;Accession: T06145
R;Bevan, M.; Vitale, D.; Liguori, R.; Argiriou, A.; De
submitted to the Protein Sequence Database, April 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease resistance protein homolog F24J7.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T06145
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A; Introns: 4/1;
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Best Local Sim
Matches 217;
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W
LLRYTCGSSVEATRAVMKHLAAVYQHGCLLGLSIAK-RPLWRQESLQSVKNTTEQEILKA 548
                                                                                                                                          DFELQDVSSVNEDVLLTTGL-------LCKYTAQRFKPKYKFFHKSFQEYTAGR--
                                                                                                                                                                                           DKIFVKLKSSYDALSVSEKEIFLDIVFTFRGANVDNVMQSLAGCGFFPRVGIEALVDKSF
                                                                                                                                                                                                                             TTLE---HTFYDLLIQKNKH-----KHKGVAASDFIRSLDHCG---DLALEGVFSHKF
                                                                                                                                                                                                                                                                       VPDQNLLELSMKFVDYANGNPLALSICGKNLKGKTPLDMKSVVL-----ELKRHLS
                                                                                                                                                                                                                                                                                                                                                  FLCEFDWLGP-----GSLIIVTSQDKQVLVQCQVNEIYKVQGLNKHESLQLFSRCAFGKD
                                                                                                                                                                                                                                                                                                                                                                                      ---EIEALIKENHRFKNMVIVTTTTECLRHIRQFGALTAEVGDMTEDSAQALIREVLIKE 316
                                                                                                                                                                                                                                                                                                                                                                                                                          FDREFQEKGFFGLLEKQL----GVNPQVTRLSILLKTLRSKRILLVLDDVR--KPLGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                PGCIIRSLGIWGMAGIGKTTLAR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLTNSIVKK---HC-LELKKMYPDDKVDEWRNALWDIADLRGGHVSSHKRSDSELVEKIV 131
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                                    VKAINLDTSNLP---FKGHIAFQHMYNLRYLT-IYSSINPTKDPDLFLPGDPQFLPPELR
                                                                                                                VTVSENRVQVN-NLIYDVGLKIINDQSDEIGMCYRFVDASNSQSLIEHKEIRESEQGYED
                                                                                                                                                                                                                                                                                                            LAEGLLLQIQK------SRCLRNLM-KTPL---FVVITCAIQMGESEFHSHTQ
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                                                                          -RLSSLLTSHEPEEVTKGNGYLQKMVSISDITSTYSS
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Pred. No. 0.16;
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disease resistance protein Hcr2-5D - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C:Accession: T30553
R:Dixon, M.S.; Hatzixanthis, K.; Jones, D.A.; Harrison, K.; Jones, J.D.G.
Plant Cell 10, 1915-1926, 1998
A;Title: The tomato Cf-5 disease resistance gene and six homologues show produced by the company of the comp
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Best Local S
Matches 147
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besidues: 1-1016 <DIX>
Cross-references: EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     814 -FPSTLLETLSEVVLLD------LENCKKLQGLPTGMSKLEFLVMLKLSG
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 147; Conserv
                            FDFFEHLPN----
                                                                           LRSL---TYLDLGENALNGSIPASLGNLNNLFMLYLYNNQL---SGSIPEEIGYLRSLTY 363
                                                                                                                                                                                                                             LLGLSIAK-----RPLWR------QESLQSVKNTTEQEI------
                                                                                                                                                                                                                                                                                                                               LTSHEPEEVTKGNGYLQKMVSIS-DITSTYSSLLRYTCGSSVEATRAVMKHLAAVYQHGC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLKNLKKMCLFHLTHLSDIGEGMDYIVKSLS----SEPCDLEEIQ-----LVSCCLSANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KLHLQGTGIRDLSSLN-HSSESQRLTRKL-----ENVSSSNQDHRKQVL 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSKLNKQDITYLGKIFSSATSLRLQIKRCAGVAGSLSLV-LSTCKNIYSLMVEASPLTIE 727
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                                                                                                                                                                              QLSGSIPEEIGYLRSLTKLSLGINFLSGSIPASLGNLNNLSRLDLYNNKLSGSIPEEIGY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AFMG-VFENLKQLVFFDFSTKEFLPDPALVRKLSQVLSKLTFLQEARLVG 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSSLLKHLEEVPQLVKLGLKNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWL 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKEVPSSLCHHISKLYKLDM------ENCERLRDLPMGMSNMKYLAVLKLS-GC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKILAQNL-HNLVKLSILDLSENYLEKDGNEALHELIDRMNVLEQLTALMLPWGCDVQGS 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLKDSS-----HLGSLPDI-----VIFESLEVLDFSGCSELEDIQGFPQNLKRLYLAKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DERHI -- TSVTNLKTLSIHDLQNQRLPGGLTDSLGNLKNLTKLIMDNIKMNEEDAIKLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDFIKLDFYGGAMASWEKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLEVTLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ININSFVECGIHLYQESTSKSALSQEFEAFFQGKSLYINSGNIPDYLFDFFEHLPNCASA 608
                                                                                                                                                                                                                                                                                                                                                                              3.1%; Score 164; DB ilarity 22.1%; Pred. No. 0:08; Conservative 115; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL:AF053998; NID:g3894392; PID:g3894393; PIDN:AAC78596.1
-CASALDFIKLDFYGGAMASWEKAAEDTGGIHM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GQLQHLRIVDLSTCKKIKSF--PKVPPSIR 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RNLKELYLAGTAVKE----
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1016;
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                          EEAPET 642
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Kinesin-related protein Eg5 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
C;Accession: A40264; 518764
R;Le Guellec, R; Paris, J; Couturier, A; Roghi, C; Philippe, M.
Mol. Cell. Biol. 11, 3395-3398, 1991
A;Title: Cloning by differential screening of a Xenopus cDNA that encodes a kinesin-r
A;Reference number: A40264; MUID:91246212
A;Accession: A40264
A;Molecule type: mRNA
A;Residues: 1-1060 <LEG>
A;Cross-references: EMBL:X54002; NID:964869; PIDN:CAA37950.1; PID:964870
A;Note: the authors translated the codon GCT for residue 784 as Leu
C;Superfamily: kinesin-related protein Eg5; kinesin motor domain homology
C;Keywords: ATP; coiled coil; microtubule binding; microsis; nucleotide binding; P-loo
F;12-358/Domain: kinesin motor domain homology <KMOTD>
F;104/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                  Matches 214;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   24 TDDLFVWNVLNREEVNIICCEKVEQDAARGII----HMILKKGSESCNLF---LKSLKEW 76
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                                                                                                                                                                                                                                              SDEEFTW----
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STLMNAYSSRSHSVFSVTIHMKETTVDG---
                                                        PSFLNFYPLGED -- IDIIFNLKSTFTEPVLWRKDQHHHRVEQLTLNGLLQALQSPCIIEG
                                                                                                                                                                            NYPLFQDLN-----GQSL----FHQTSEG----DLDDLAQDLKD-LYH---
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                                                                                                                       NEELFDLLSPSPDVGERLQMFDDPRNKRGVIIKGLEEISVHNKDEVYHILERGAARRKTA
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                                                                                                                                                                                                                                                                                                                                                                  Conservative 155;
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                                                                                                                                                                                                                                           -----EQDPLAGIIPRTLHQIFEKLSENGTEFSVKVSLLEIY 157
                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 164; DB 1
20.3%; Pred. No. 0.085;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EIRILGAFFGK -- NPLK ---
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                     383;
   EELVKIGKLNLVD---
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1060;
                                                                                                                                                                                                                                                                                                                                                                     Indels 302;
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      -LAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       473 FVVSAFETTEKKLHGT-ANKL-----LSTYRETTRDVSGLHEKLDRKKAVDQHNFQVHE 525
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                                                                                                 963 LESISSVIS-EAVEPPVEQDSLEDEPPVAVNDSVISERSCIDLSMTCQEKGGIRFFQQKK 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        725 QLNLLGMETQQQFSGFLSKGGKLQKSVGSLQQDLDLVSSEAIECISSHHKKLAEQSQDVA 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 AMASWEKAAEDTGGIHMEEAPETYIPSRAVSLFFNWKQEFRTLE------ 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526 NFAE-QMDRRFSVIQRTVDDYSV-KQQGMLDFYTNSIDDLLGASSSRLSATAS----- 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            664 ------VTLRDFS------KLNK------QDITYLG-------KIFSSATSLR 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 SRCLRNLMKTPLFVVITCA--IQMGESEFHSHTQTTLFHTFYDLLIQKNKHKHKGVAASD 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 GTIRKQTFMAML----LKLRQRVLFLLDGYNEFKP-QNCPEI-----EALIKENHRFKN 273
                                                                                                                                                                                                                                                  784 AEGLKN-LKKMCLFHLTHL-SDIGEG-----MDYIVKSL--SSEPCDL------EE 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   262 SENIGRSGAVDKRAREAGNINQSLLTLGRVITALVERTPHIPYRESKLTRILQDSL----
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                                               -----NEALHELIDRMNVLEQ----LTALMLP 887
                                                                                                                                                                                                                                                                                                                                                      DMNSF--FTEHSRSLHKLRLDSSSALSSIQSEYESLKEDIATAQSMHSEGVNNLISSLQN 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIRSLDHCGDLALEGVFSHKFDFELQDVSSVNEDVLLTTGLLCKYTAQRFKPKYKF-FHK 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SQAKGDLQQLMAAHRTGLEEALRSDLLPVVTAVLDLNSHLSHCLQNFLIVADKIDSHKE 666
                                                                                                                                                 IQLVSCCLSANAVK------ILAQNLHNLVKLSILDLSENYLEKDG------
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Search completed: March 25, 2002, 10:56:44 Job time: 104 sec

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Database sequences: 351203
Database length: 113238999
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                                                       _6/Ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-07754A-5 + 130.00
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_6/Ptodata/2/ina/5B_COMB.seq:US-08-416-603-1 + 129.00 195.
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; ORGANISM: HO
US-08-836-134-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-836-134-1 from: 1 to:
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                                                                              1622 AGCTTATACCAGCGCCAGTTTCCGCCACATGTCTTTGCTTGATATCTCTT 1671
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                       145 sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG
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                                                                                                                                  AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi 145
                                                                                                                                                                                         CCGATCTGGCCACGGACCACTTGCTGGGCTGTGATCTGTCTATT..... 1715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....LeuAlaGlnAspLeuLysAs
                                                                                                                                                                                                                                                .....TyrProLeuGlyGluAspIleAspIleIlePhe 128
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5. 6020127
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Mahadevan, Mani S.
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107 1571 100

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APPLICANT: Roy, Natalie
APPLICANT: IXeda, Joh-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence
Patent No. 6020127
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/08/836,134A
CURRENT FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
SEQ ID: 00 1
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2655	SPIONYSTYLNYSPHENEHISLYSSERFINEGIOLUTYTTINAGIYA	2606
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ώ ω 0 0	alLeuLeuThrThrGlyLe          	420
419 2555	ysPheAspPheGluLeuGlnAspValSerSerValAsnGluAsp    :::   ::: 	405 2506
405 2505	SCYSGLYASPLE       :::   CTGTGGTGAGCT	389 2456
388 2455	sHisLysGl	373 2424
372 2423	erHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 	356 2374
356 23 <b>7</b> 3	uPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS        :: 	339 2324
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308 2223	rAlaGluValGlyAspMetThrGluAs     :::  CTAGAGATCCAAGCATTTCCCTTTTA	291 2174
291 2173	ValleValThrThrThrThrGluCysLeuArgHisIleArgGlnPheGl::::::::::::::::::::::::::::::::::::	275 2124
274 2123	luileGluâlaLeuileLysGluâsnHisargPheLysasnM 	258 2079
258 2078	LLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnC	243 2033
243 2032	IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa ::: :::::: :::  ::::::   GTTACTGAAATGTGCATGAGGAACATTATCCAGCAGTTAAAGAATCAGGT	227 1983
226 1982	lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr	210 1933
210 1932	rLysPheLysPheValPhePheLeuArgLeuSerArgAlaGlnG::::    ::::            ::: 	195 1883
195 1882	LeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTh    ::::::      :::	179 1833
178 1832	ProCysI GTCATGI	162 1783
1782	CAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGCAACTTGA	1743

680	3 uValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL	66
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646 3395	1 hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer 1 hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer 2 TTAGTACTGGCTAATGGAAACTTTCTCCAAAGACTAGTAAGATTCCC	63 334
3348	GATAATGTAAAGAGCTATATGGATATGCAGCGCAGGGCATCACCAGACC	329
631	1GluAspT	62
625 3298	8 GlyGlyAlametAlaSerTrpGlu ::::::       :::	61: 324:
3248	SACAAATCACAGGTGCCAACTATAGATCAGGACTATGCT	319
617	nCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr	60
3198	CTCAATACGAGGAAATAAGACATCACCCAGAGCACATTTTTCAGTTCTGG	3149
603	ıHisLeuP	59:
597 3148	4 TyrLeuPheAsp	59. 309.
3098	AATTCCTTCAAGGGAGAACACTGACTTTGGGTGCGCTTAACTTACAG	3052
593	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp	577
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561	/alGluCysGlyIleHisLeu	55
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539 2904	3 rLeuGlnSerValLysAsn	285 285
2854	AAAGAGTC	284
533	CysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSe	517
2846	aagcagggccaaaattgtgtctcatttgctccatttagtggataac	2800
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503 2799	6 TTYrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrA	48i 275i
486 2755	0 GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh       ::   :::::        6 GGACTGTATCATTTGAAACAAATCAACTCACCCATGATGACTGTAAGCGC	47) 270)
2705	TTG	265
469	euThrSerHisGluProGluGluValThrLys	45

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seq_documentation_block:
    Sequence 1, Application US/08930996A
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Applica Patent No. 6100449
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                            APPLICANT: PARÂN, Ilan
APPLICANT: ZAMIR, Danilel
TITLE OF INVENTION: A GENE FAMILY FROM THE 12 FUSARIUM RESISTANCE
TITLE OF INVENTION: LOCUS OF TOMATO AND USE THEREOF FOR TRANSFORMATION AND
TITLE OF INVENTION: SELECTIVE BREEDING OF TOMATO AND RELATED PLANTS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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COUNTRY:
                 CITY: Washington STATE: D.C.
                                                                 STREET:
                                                                                        ADDRESSEE:
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                                                                 419 Seventh Street, N.W.,
                                                                                        BROWDY AND NEIMARK
                                                                    Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801
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135 748	spllelle	125 699
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95 610	roLeuPheGlnAspLeuAsnGlyGlnSerLeuPheHisGlnThrSerGlu::::::	79 579
79 ·	ySerGluSerCysAsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrP	529
62 528	ValGluGlnAspAlaAlaArgGlyIleIleHisMetIleLeuLysLysGl	46 479
45 478	snValLeuAsnArgGluGluValAsnIleIleCysCysGluLys:::   :::   :::   :::   :::    :::     :::	31 429
31 428	TGATCTGCTCAACATGTTTCGGAAGCATACAGATGATGTAGACTCTTTG	17 379
16 378	PhelleLysAspAsnSerArgAlaLeuIleGlnArgMetGly    ::::::   :::::   :::::   TTTCTCTCCTCAGCTTTGAATGTTCTGTTTGATAGGCTTGCTCCTAATGG	329 3
	eg 1/1 to: US-08-930-996A-1 from: 1 to: 4946	Align s
	.97-089-2 x US-08-930-996A-1	alignmen US-09-6
	Length: 1303 Quality: 177.50 Ratio: 0.310 Ratio: 0.389 Percent Identity: 18.649	alignmen Percent
	NAME/KEY: CDS LOCATION: 2993958 30-996A-1	6-80-SI
	COLE TYPE: URE:	MO FE
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	ENCE CHARA	SE
	DATE: 13-AP	0
	LING DATE: 15-APR-1996 R APPLICATION DATA:	PR
	PLICATION DATA: ATION NUMBER: PCT	'n
	LICATION NUMBER: UING DATE: 09-DEC-1	
	S L	C C
	TYPE: Floppy disk TER: IBM PC compatible	
	20004 READABLE	co.

356 1594	16AlaIleGlnMetGlyGluSerGluPheHisSer	346 1545
345 1544	9 gCysLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCys.	329 1495
329 1494	3 LeuIleLysGluLeuAlaGluGlyLeuLeuLeuGlnIleGlnLysSerAr :::                       ::: :::::: ::::::	313 1448
312 1447	6 luvalGlyAspMetThrGluAspSerAlaGlnAlaLeuIleArgGluVal	296 1404
296 1403	4 ACGACATTCATTAGAGCACAAGGATCCCAAGGAACATCCAGAAT	294 1354
	2 AlaLeu	0 9
291 1303	5 alllevalThrThrThrGluCysLeuArgHislleArgGlnPheGly :::	275 1254
275 1253	7 uAsnHisArgPheLysAsnMetv :::   ::: 7AGAAATCTTTTTTTACAAGGGGATATAGGAAGTAAGA	267 1217
267 1216	1 ASNGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGl	251 1187
250 1186	0 rgGlnArgValLeuPheLeuLeuAspGlyTyr ::::	240 1137
240 1136	4 roGlyThrIleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuA :::::	224 1087
224 1086	5 rLeuCysAspGlnLeuLeuAspIleP                         0 ATTGGATCAACTGACTTGAAGGCTGATGACAATCTTAATCAGCTACA	215 1040
215 1039	9 PheValPhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluTh    :::      :::	199 990
198 989	6 rpGlySerGlyLysCysLysAlaLeuThrLysPheLys :::   :	186 948
186 947	0 GluSerGlyLysGlyLysSerThr.LeuLeuGlnArgIleAlaMetLeuT:::          ::: ::::   :::   :::   ::   :::  :::   ::   :::  :::   :::   :::   :::  :::  :::  :::  :::   :::   :::   ::	170 899
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13 <i>1</i> 798	9 TCGACCAAACAAGAAACTAGAACACCTTCAACTTCTTTGGTTGATGATTC	749

276		
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559	CysGlyIle	
543 2423		
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510 2326	508Hisleuala !	
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362	362	
1644	35/ HISTORGINTALTINEU	

2 !		
778	euLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGlu (euLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGlu (euLysAsnCrarrande)	762 3198
3197	PHENDATIANS THAT GLEUPT OUT YGLY LEUT DIAS SEE LENGLYKSDL  :::::	3148
745 3147	gn.siterniservaltiirksiileulystiirleuserlehtset	9 6
3097	PAATAAAGATATCTGGTTGCCCAAAATTGAAATTGGAGGCGCCAGTTGGT	<u> </u>
728	Asp	72
727 3047	SLYSASDILETYRSerLeuMetValGluAlaSerProLeuThrIleGlu.     ::::::	2998
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702 2947	erAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGly :::   :::    :::    :::::: AAACTTTCCATTAAAATTGCCCTGAGCTCAGTTTG	686 2912
9		
686	${\tt eSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLysIlePheSerS}$	669
669 2911	GluPheArgThrLeuGluValThrLeuArgAspPh	658 2879
2878		2864
657	31n	643
643 2863	salaalaGluaspThrGlyGlyIleHisMetGluGluAlaProGluThrT	626 2818
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597 2673	SerGlyAsnIleProAspTyrLeuPheAsp	588 2624
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2573	TGAAAGCATTAGTGCTGACAATTCACAAAACAGAAAGAGACATACTTGATG	2524
்ப்	GATGAGGAGAAGAATCATGTTGAGCAATTATCATTGGAGTGGAG	. 7

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947 3650	YLYSASnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsn    :::	932 3604
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915 3559	YSHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLys ::   :::      :::   ::: AACATATTGAACATTGGGAGTTGCCTTCCTCTATTCAG	901 3522
901 3521	tLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuL :::	885 3499
885 3498	HisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMe	869 3473
868 3472	SpLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAlaLeu	854 3429
854 3428	llysileLeuAlaGlnAsnLeuHisAsnLeuVallysLeuSerileLeuA :::    ::::	837 3388
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seq\_documentation\_block:
 Sequence 1, Application US/09180439
; Patent No. 6225532
; GENERAL INFORMATION:
 APPLICANT: Dixon, Mark S
 APPLICANT: Hatzixanthis, Kostas
; APPLICANT: Jones, David A
; APPLICANT: Jones, Jonathan DG
; TITLE OF INVENTION: plant pathogen resistance genes and uses thereof

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FILE REFERENCE: 620 - 53
CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER FILING DATE: 1997-05-08
EARLIER FILING DATE: 1996-05-09
EARLIER APPLICATION NUMBER: GB 961924.5
EARLIER APPLICATION NUMBER: GB 961924.5
EARLIER APPLICATION NUMBER: GB 961924.5
SOFTMARE: Patentin Ver. 2.0
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 3979
TYPE: DNA
ORGANISM: Lycopersicon esculentum
US-09-180-439-1
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US-09-697-089-2 x US-09-180-439-1
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   Quality:
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cent Similarity:
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                                                 1640 TTCATTGGGGAATCTAAACAACTTGTCTAGGTTGGATCTTTACAATAATA 1689
                                                                                                                                                   1590 CTTACTTACCTAGATTTGGGTGAGAATGCTCTTAATGGCTCTATTCCTTC 1639
                                                                                                                                                                                                                                                1464 GGTATCAACTTTCTTAGTGGTTCCATTCCTGCTTCATTGGGGAATCTAAA 1513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1450 CTAAG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1514 CAACTTGTCTAGG.....
620 laMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMet 636
                                                                             604 nCysAlaSerAlaLeuAspPheIle...LysLeuAspPheTyrGlyGlyA 620
                                                                                                                                                                                                                                                                                                                                                                              571 ....LeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrI 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             558 GlyIleHisLeuTyrGlnGluSerThrSerLysSerAla...... 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 hrGluGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCys 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 aLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThrT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 HisLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAl 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491 euArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLys 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   459 LeuThrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGl 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....TTTCTTAGTGGTTCCATTCCTGCTTCATTGGGGAATCTGAAC 1370
                                                                                                                                                                                               ......PheaspPhePheGluHis.....LeuProAs 604
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0.533
50.548
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Gaps: 38
Percent Identity: 23.005
                                                                                                                                                                                                                                                                                                                                                    ......TTGGATCTTTACA 1539
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3979
; TYPE: DNA
; ORGANISM: Lýcopersicon esculentum
US-09-180-439-2
alignment_block:
                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09180439 Patent No. 6225532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Dixon, Mark S
APPLICANT: Hatzixanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
APPLICANT: Jones, Jonathan DG
FITLE OF INVENTION: Plant pathogen resistance
FILE REFERENCE: 620 - 53
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: GB 9619924.5 EARLIER FILING DATE: 1996-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: GB 'EARLIER FILING DATE: 1996-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2591 CAAAAAGCTGCAAGTTCTTGATTTAGGAGACAATCAACTCAACGACACAT 2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2541 TTGCATGGCAATGAACTAGCAGATGAAATCCCTCGGTCTTTGGACAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2641 TTCCCATGTGGTTGGGAACTTTGCCAGAGCTGAGAGTTTTAAGGTTGACA 2690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2493 ..ACTCTTCCAACAAATTTTAGCATTGGATGTTCACTGATAAGTCTCAAC 2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            981 oAlaLeuVal......ArgLysLeuSerGlnValLeuS 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       970 PheAspPheSerThrLysGlu.................PheLeuProAspPr 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       953 lyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhe 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         931 PheGlyLys.....AsnProLeuLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTTGTACACAATTATC 2948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erLysLeuThrPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGGTAGTTGTGACAAAGGGATTGGAGCTTGAAATTGTGAGAATTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTGATCTCCGAATCATAGATCTCTCTCGCAATGCATTCTCGCAAGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGAATAAATTGCATGGACCTATAAGATCATCAGGGGCTGAAATCATGTT 2740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......GluIleArgIleLeuGlyAlaPhe
                                                                                                     Quality:
                                                                          Ratio:
                                                 172.00
0.533
50.548
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                                                 Percent Identity:
                                                                          Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes and uses thereof
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Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1734 CTTACTTACCTAGATTTGGGTGAGAATGCTCTTAATGGCTCTATTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1464 GGTATCAACTTTCTTAGTGGTTCCATTCCTGCTTCATTGGGGAATCTAAA 1513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1690 AGCTTTCTGGC.....TCTATTCCTGAAGAAATAGGTTACCTAAGGTCT 173:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 laMetAlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIleHisMet 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1540 ATAATAAGCTTTCTGGCTCTATTCCTGAAGAAATAGGTTACCTAAGGTCT 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1514 CAACTTGTCTAGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 nCysAlaSerAlaLeuAspPheIle...LysLeuAspPheTyrGlyGlyA 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 leAsn.....SerGlyAsnIleProAsp......TyrLeu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 hrGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCys 557
713 snIleTyrSerLeuMetValGluAlaSerProLeuThr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 aLysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThrT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 euArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLys 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 nLysMetValSerIleSer...AspIleThrSerThrTyrSerSerLeuL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 LeuThrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGl 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCATTGGGGAATCTG......AACAACTTGTTTATGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuG 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTACTTACCTAGATTTGGGTGAGAATGCTCTTAATGGCTCTATTCCTTC 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyIleHisLeuTyrGlnGluSerThrSerLysSerAla.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisteuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAl 524
                                                          .....TCTCTTAATGGCTCTATTCCTGCTTCATTGGGGAATCTGAACA 194;
                                                                                                               {\tt gCysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLysA}
                                                                                                                                                                                                                                                                                                                                                      luValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyr 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCATTGGGGAATCTAAACAACTTGTCTAGGTTGGATCTTTACAATAATA 1689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....LeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTyrI 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....PheAspPhePheGluHis.....LeuProAs 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......CCTGAAGAAATAGGTTACCTAAGGTCACTTA 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....GluGluAlaProGluThrTyrIleProSe 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: US-09-180-439-2
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   ..Ile
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969	953 lyTrpLeuAlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPhe
953 2789	938AsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspG ::::::::::::::::::::::::::::::::::::
937 2740	931 PheGlyLysAsnProLeuLys
930 2690	923
922 2640	908GInLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThr. :::                  :: ::   ::       2591 CAAAAAGCTGCAAGTTCTTGATTTAGGAGACAATCAACTCAACGACACAT
907 2590	901 LyshisLeuGluGluValPro
900 2540	884 eumetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu
884 2492	867 aLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaL :::::::    :::    2450 TAGCCTCCAGGTTTTTGATATGCAGAATAACAAACTTTCTGGG.
867 2449	856 SerGluAsnTyrLeuGluLysAspGlyAsnGluAl ::::::                   ::
855 2399	839 leLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeu
839 2349	823 uGluIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysI ::::::::::::::::::::::::::::::::::
823 2305	819
818 2255	806 luGlyMetAspTyrIleValLysSerLeuSerSerGlu
806 2205	792 sMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyG::::
792 2173	777 GluGluAspAlaTleLysLeuAlaGluGlyLeuLysAsnLeuLysLy :::       :::::      ::: 2130GGCTCTATTCCTGCTTCATTTGGCAATATGAGAAATCTGCAAAC
776 2129	760 lyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMetAsn         :::     ::::    :::       ::::::
760 2079	743 eHisaspLeuGlnasnGlnargLeuProGlyGlyLeuThraspSerLeuG
743 <sup>*</sup> 2033	727 GluaspGluargHisIleThrSerValThrAsnLeuLysThrLeuSerIl
1997	::::::     ::: ::    :::: 1948 ACTTGTTTATGTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATTCCT

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-353-585-4
US-09-353-585-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09353585 Patent No. 6287865 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2932 CTTTGTACACAATTATC 2948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2882 GGTGGTAGTTGTGACAAAGGGATTGGAGCTTGAAATTGTGAGAATTCTGT 2931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2832 GTTGATAAAACAATGGAGGAACCAAGTTATGAAAGCTATTACGATGACTC 2881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2790 .....TTACCAACGAGTCTATTTGAACATTTGAAAGGGATGAGGACA 2831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   992 erLysLeuThrPheLeu 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         981 oAlaLeuVal......ArgLysLeuSerGlnValLeuS 992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/353,585

FILING DATE: 15-Jul-1999

CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C120

1/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones, David A
Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
thereof
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 9506658.5
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: MS MARY J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-0CT-1997
APPLICATION NUMBER: PCT/GB96/00785
APPLICATION NUMBER: PCT/GB96/00785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
                                                                       ORIGINAL SOURCE:
ORGANISM: Tomato
                                                                                                                                                   STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dixon, Mark S
                     SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                ANTI-SENSE: NO
                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                      STRAIN: Cf2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
STATE: Virginia
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alignmen Percent	lignment_scores:  Quality: 165.00 Ratio: 0.546 Percent Similarity: 46.822 Reserved Similarity: 46.822	
alignmen US-09-6	t_block: 97-089-2 x US-09-353-585-4	
Align s		
425 410	GlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPh 4	41 41
441 442	rgArgLeuSerSerL 4	58 54
458 455	roGluGluValThrLysGlyAsnGlyTyrLeu 4   :::   :::  TAAAGAAATAGTTACCTA 4	74 90
475 491	ThrTyrSerSerLeuLe 4	91 32
491 533	uArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysH 5: :::   ::: ;:::::::::::::::::::::::::::	08
508 567	isLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAla 5 ::   :::	24
525 614	AC 6	41
541 646	rGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysG 5:	58 58
558 659	laLeuSerGlnGlu 5	74 82
575 683	PheGlualaPhePheGl 58 :::     ATTCCTGCTTCATTGGGGAATATGAACAACTTGTCTTTTTTTT	80 32
580 733	nGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp	94
594 774	yrLeuPheAspPhePheGluHisLeuProAsnCys 60	23
606 824	AlaSerAlaLeuAspPheIleLysLe 61 :::	14 73
614 874	uAspPheTyrGlyGlyAlaMetAlaSerTrpGluLysAlaAlaGluAspT 631	31
631 912	hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSerArg 647	47
648	AlaValSerLeuPhePheAsnTrpLySGlnGluPheArgThrLeuGluVa 66	44.

664	ThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuG	681
937	TGAGAATGCTCTTAAT	964
681	${\tt lyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgCys}$	697
964		964
698		714
965	THE CTGCTTCATTGGGGAATCTGAAAAACTT	1002
714	TyrSerLeuMetValGluAlaSerProLeuThrIleGluAspGluArgH	731
1003	GTCTAGGTTGAATCTTGTTAATAATCAGCTTTCTGGCTCTATTCCT	1048
731		747
1049	GCTTCATTGGGGAATCTGAACAACTTGTCTATGTTGTATCTTTAC	1093
748		764
1094	CTGCTTCATTGGGGAATCTGAACAA	1143
764	laI	781
1144	AATCAGCTTTCTGGCTCTATTCCTG	1193
	GlyLeuLysAsnLeuLysLysMetCysLeuPheHis	797
1194	AATCTGAACAACTTGTCTAGGTTGTATCTCTACAAT	1240
798		813
01.4	1,71	123
1291	TACTTATCTAGATTTGAGTAATAACTCCATTAATGGATTTATTCCTGCTT	1340
822		826
1341	TTGGCTTTTTGTTTCTTTATGAAAATCAG	1390
827		843
1391	GTTCCTGAAGA	1413
843		860
1414	AATAGGTTACCTAAGGTCTCTTAATGTCCTTGATTTGAGTGAG	1463
1464	euGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsn (	876
877		893
1502	AACTTGTCTAGGTTGAATCTTGTTAA 1	1527
893 1528	nGlySerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuV 9 ::::::      :::	910 1571
910 1572	alLysLeuGlyLeuLysAsnTrpArgLeuThrAspThrGluIleArg 9 :::   :::::::::::::::::::::::::::::::	925
926	eLeuGlyAlaPhePheGlyLysAs :::	942
1616	:	1659

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Sequence 1, Application US/09353585
Patent No. 6287865
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-353-585-1
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                                                                                                                                                                                                                    TELEFAX: (703) 81
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FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/ACENT INFORMATION:
NAME: MS MATY J Wilson
REGISTRATION NUMBER: 32,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysLeuSerGlnValLeuSerLysLeuThrPheLeu
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ORIGINAL SOURCE:
ORGANISM: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-JUl-1999
CLASSIFICATION: C11N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 6471 base pairs
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Plant pathogen resistance genes and thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....AlaPheMetGlyValPheGluAsnLeuLysGlnLeuValPh
                                                HYPOTHETICAL: NO
                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Nixon & Vanderhye PC STREET: 8th Floor, 1100 No. 6287865th
                                                                                                 TOPOLOGY:
                                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 620-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22201-4714
                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones, Jonathan DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jones, David A
                                                                       DNA (genomic)
                                                                                                 linear
                                                                                                                                                                                                                                                816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-697-089-2 x US-09-353-585-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-353-585-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-353-585-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2094 GGTTTACTAGCCAAGCTTCAGATCATCCGC.....AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2251 ACTTGTCTTTTTGTATCTTTACAATAATCAGCTTTCTGGCTCTATT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2139 ..TTAAATGGATTTATTCCTAAAGAAATA........GGTTACCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2126 ATTTCACAATCAA.....
                      2458 ACCTAAGATCTCTTACTTACCTAGATTTGAGTGAGAATGCTCTTAATGGC
                                                                                                                                                                                                                    2417 TGGAAATCAGCTT.....TCTGGCTCTATTCCTGAAGAAATATGTT 2457
                                                                                                                                                                                                                                                                                                                       2367 ATTCCTGCTTCATTGGGGAATATGAACAACTTGTCTTTTTTGTTTCTTTA 2416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              458 euLeuThrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeu 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 ePheHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerL 458
                                                                                                                                                                   594 yrLeu.....PheAspPhePheGluHisLeuProAsnCys 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 rGluGlnGluIleLeuLysAlaIleAsnIleAsnSerPheValGluCysG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 LysArgProLeuTrpArgGlnGluSerLeuGlnSerValLysAsnThrTh 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 isLeuAlaAlaValTyrGlnHisGlyCysLeuLeuGlyLeuSerIleAla 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 uArgTyrThrCysGlySerSerValGluAlaThrArgAlaValMetLysH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 GlyLeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPh 441
                                                                  606 Ala.....SerAlaLeuAspPheIleLysLe
                                                                                                                                                                                                                                                               580 nGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp...... 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    558 lyIleHisLeuTyrGlnGluSerThrSerLysSerAlaLeuSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnLysMetValSerIleSerAspIleThrSerThrTyrSerSerLeuLe
                                                                                                                                                                                                                                                                                                                                                                PheGluAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGCTAGATTTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....CCTGAAGAATAAGTTACCTAAGATCTCTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGTCTCTTACTAAGCTATCT...TTGGGTATCAACTTTCTTAGT....
                                                                                                                                                                                                                                                                                                                                                                                                                 .....AGTGATAATGCTCTTAATGGCTCT 2366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: mat_peptide LOCATION: 1754..5012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: sig_peptide LOCATION: 1677..1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN: Cf2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.546
46.822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .GGTTCCATTCCTGCTTCAGTGGGGAATCTGAACA 2250
                                                                                                                                                                                                                                                                                                                                                              .....PhePheGl 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 21.395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N⊙:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>.
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614 2507 574

2342

2329

2297

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2216 491 2174

2138

910	sLeuGluGluVa	893
893 3211	uPr	877 3186
876 3185	uGluLysAspGlyAsnGluAlaLeuHisGluLeuI1 	0 4
860 3147	AsnLeuValLysLeuSerIleLeuAsp      :::   :::::        TACCTAAGGTCTCTTAATGTCCTTGAT	843 3098
843 3097	AsnAlaVa	827 3075
826 3074	CAATATGAGCAACTTGGCTTTTTTGT	822 3025
821 3024	SerLeuSerSerGluProCysAsp	814 2975
813 2974	rHisLeuSerAspIleGlyGluGlyMetAspTyrIleVa 	798 2925
797 2924	leLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHis :::   :::    ::::    :::::    :::::    :::::    ::::	781 2878
781 2877	SLeuIleMetAspAsnIleLysMetAsnGluGluAs 	764 2828
764 2827	SnG   -	748 2778
747 2777	hrSerValThrasnLeuLysThrLeuSerIleHisAspLeuG ::   :::       :::::      ::: CTTCATTGGGGAATCTGAACAACTTGTCTATGTTGTATCTTT	731 2733
731 2732	eTyrSerLeumetValGluAlaSerProLeuThrIleGluAspGluArgH :::         ::: :::	714 2687
714 2686	aG1ySerLeuSerLeuValLeuSerThrCy       ::: .GGCTCTATTCCTGCTTCATTGGGGAATCT	698 2649
2648		2648
697	ePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgC	681
681 2648	uArgAspPheSerLysLeuAsnLysGlnAsp :::          TTTGAGTGAGAATGCTCTTAAT	664 2621
664 2620	euPhePheAsnTrpLysGlnGluPheArgThrLeu    :::    AGATCTCTT	648 2607
647 2606	yGlyIleHisMetGluGluAlaProGl   	631 2596
2595	TTCTGGCTCTAT	2558

IS	IMENTATION_block: INCO 7, APPLICATION US/09180 L NO. 622532 L INFORMATION: ICANT: Dixon, Mark S ICANT: Dixon, Mark S ICANT: David A ICANT: Jones, David A ICANT: Jones, David A ICANT: Jones, Jonathan DG EOF INVENTION: Plant patho REFERENCE: 620 - 53 ENY APPLICATION NUMBER: US/ ENY TELLING DATE: 1998-12-06 IER FILING DATE: 1998-05-09 IER APPLICATION NUMBER: GB IER FILING DATE: 1996-05-09 IER APPLICATION NUMBER: GB IER FILING DATE: 1996-09-24 ARE: PatentIN Ver. 2.0 ARABE: PatentIN Ver. 2.0 ONO 7 STH: 4123 STH: 4124 STH: 412	seq_doc ; Seque ; Paten ; Gener ; AppL ; AppL ; AppL ; AppL ; AppL ; TITL ; FILE ; CURR ; CURR ; EARL ; ORG ; ORG US-09-1 alignme US-09-1 45:
B_COMB.seq:US-09-180-439-7	<pre>ime: /cgn2_6/ptodata/2/ina/6B_</pre>	seq_name:
euThrPheLeu 997      ::    !TTACTTATCTA 3560	986 ysLeuSerGlnValLeuSerLysLeuThrP       :::      : 534GGTTACTTGAGTTCTCTTACTT	9 35
eLeuProAspProAlaLeuValArgL 986 	369 ePheAspPheSerThrLysGluPheLeuProA ::::::::::::::::::::::::::::::::::::	· 9 34
PheGluAsnLeuLysGlnLeuValPh 969 	956AlaPheMetGlyValPheGluAsnLeuLysGln      :::   ::::     ::::  444 TCTATTCCTGCTTCATTGGGGAATCTGAACAACTTGTCTATG	9 34
GTTTGAGTGAGAATGCTCTTAATGGC 3443	54 rpleu	33 9
GlyT 95     : TTCCTGAAGAATAGGTT 33	4 4	33 9
AsnProLeuLysAsnPheGlnGlnLe 942	26 IleLeuGlyAlaPhePheGlyLys :::            ::: 00 TCTATTCCTGCTTCATTCGGGAAT	33
PARGLEUTHRASPTHRG1uIleArg 925	10 allysLeuGlyLeuLysAsnTr :::   ::::: 56 GGTCTCTTAATGTCCTTGAT	32 32
TGAAGAAATAGGTTACCTAA 3255	:::::::       ::: 12 TAATCAGCTTTCTGGCTCTATTCCT	32

2110	TCTATTCCTGCTTCATTGGGGAATCTGAACAACTTGTTTATGTTGTATCT	2061
719	SerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLeuMetV	
702 2060	erAlaThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGly	686 2020
686 2019	eSerLys :    TTCTGGC	669 1982
669 1981	PheAsnTrpLysGlnGluPheArgThrLeuGluValThrLe	653 1944
652 1943	GluGluAlaProGluThrTyrIleProSerArgAlaValSerLeuPhe	637 1897
636 1896	SAlaAlaGluAspThrGlyGlyIleHisMet	626 1847
626 1846	AspPheIleLysLeuAspPheTyrGlyGlyAlaMetAlaSerTr :::::::::::::::::::::::::::::::::::	610 1803
609 1802	heGluHisLeuProAsn	599 1753
599 1752	nIleProAspTyrLeuPheAspPheP::      :::	590 1703
590 1702	GluPheGluAlaPhePheGlnGlyLysSerLeu     	574 1662
573 1661	leHisLeuTyrGlnGluSerT ::: ::: AGAATGCTCTTAATGGCTCTATTCCTG	559 1612
559 1611	AATAGGTTACCTAAGGTCTCTT.	546 1571
545 1570	ThrGluGlnGluIle	541 1521
540 1520	ACTTTCTTAGTGGTTCCATTCCTGCTTCATT	531 1471
530 1470	aLys ::: TGAAGAAATAGG	524 1421
524 1420	HisLeuAlaAlaValTyrGlnHisGlyCysLeuI :::   :::  ACTTGTCTTTTTTGTATCTTTACAATAATCAGC	508 1371
507 1370	euArgTyrThrCysGlySerSerValGluAlaT ::::::   :::    :TTTCTTAGTGGTTCCATTCCTGCTT	491 1329
1328	GTCTCTTACTAAGCTATCTTTGGATATCAAC	1298

976	ASDP	959
2944	GATCTCTCTCGCAATGCATTCTCGCAAGACTTACCAACGAG	2904
n io	:::::: TATAAGATCATCAGGGGCTGAAATCATGTTTCCTGATCTCCGAA	<u>-</u> ر
42	LeuLysAsnPheGlnGlnL	93
935 2853	GluIleArgIleLeuGlyAlaPhePheGlyLysAsnP     :::    :::    	923 2804
922 2803	GlyLeuLysAsnTrpArgLeuThrAspThr	913 2754
912 2753	euGluGluValPro	903 2704
903 2703	SASPValGInGlySerLeuSerSerLeuLeuLysHisL ::::::              TAGCATTGGATGTTCACTGATAAGTCTCAACTTGCATGGCAATGAACTAG	890 2654
890 2653	ArgMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTrpGlyCy :::    :::::   :::::   ATGCAGAATAACAAACTTTCTGGGACTCTTCCAACAAATTT	874 2613
873 2612	ysaspGlyasnGlualaLeuHisGluLeuIleAsp               ::: ::::::	862 2563
862 2562	SASnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGluL       :::::   :::            CAATTTAACATCACTAAAAATACTTGATTTTGGCAGAAACAATCTGGAGG	845 2513
845 2512	CysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHi :::   :::   :::    ::::::::::::::::::	830 2469
829 2468		819 2419
818 2418	LLysSerLeuSerSerGlu	812 2369
812 2368	IleGlyGluGlyMetAspTy            :::: TCTCATTGGGGAAATTCCTTCATT	799 2322
798 2321	euAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeu :::      :::::      ::: ::: CTTCATTTGGCAATATGAGAAATCTGCAAACTCTG	783 2287
783 2286	rLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysL::::   :::   :::    :::    :::    :::     :::     :::     :::     :::     :::	766 2243
766 2242	rAspSerLe        GCTTCATT	750 2193
749 2192	hrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAsnGln::   :::	733 2161
733 2160	lGlualaSerProLeuThrIleGluAspGluArgHisIleT::::::::::::::::::::::::::::::::::::	719 2111

::::        :::
976 luPheLeuProAspProAlaLeuVal 984
985ArgLysLeuSerGlnValLeuSerLysLeuThrPheLeu 997 :::::: ::::::
q_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-353-700-2
<pre>q_documentation_block: q_documentation_block: Sequence 2, Application US/08353700 Patent No. 5599919 GENERAL INFORMATION: APPLICANT: YEN, TIMOTHY J. APPLICANT: YEN, TIMOTHY J. APPLICANT: YEN, TIMOTHY J. APPLICANT: YEN, TIMOTHY J. APPLICANT: YEN, TENOME B. APPLICANT: YEN, TENOME B. APPLICANT: YEN, TENOME B. APPLICANT: YEN, TENOME B. TITLE OF INVENTION: TRANSIENTLY-EXPRESSED KINETOCHORE PROTEIN, TITLE OF INVENTION: AND METHODS OF USE NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: DANN, DORFMAN, HERRELL AND SKILLMAN STREET: 1601 MARKET STREET, SUITE 720</pre>
COUNTRY: USA COUNTRY: USA ZIP: 19103-2307 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION UMBER: US/08/353,700 FILING DATE: 09-DEC-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: REED, JANET E. REGISTRATION NUMBER: 36,252 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:
TELEPAN: (215) 503-4100 TELEPAX: (215) 503-4100 TELEPAX: (215) 503-4044 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENCTH: 10136 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO
ignment_scores:  Quality: 149.50  Ratio: 0.266  Gaps: 52  ercent Similarity: 48.702  Percent Identity: 18.426
ignment_block: s-09-697-089-2 x Us-08-353-700-2
lign seg 1/1 to: US-08-353-700-2 from: 1 to: 10136
39 ASNI1eIleCysCysGluLysValGluGlnAspAlaAlaArgGlyIleI1 55

بر 5	uMetLvsThrProLeuPheValValIleThrCvsAlaIleGlnMetGlvG	334
3028	TTT	2979
334	uLeuGlnIleGlnLysSerArgCysLeuArgAs	318
317 2978	luAspSeralaGlnAlaLeuIleArgGluValLeuIleLysGluLeu ::::::           ::    :: .:GAAACTGAGCAGGCAGAGATTCAAGAATTAAAAAAGAGCAACCATCTA	302 2931
2930	AGGAAAAGAGCTGCAACTTTTAAATGATAAGGTA	9
302	LIBCICACCABAAIBIIBIIBCIBAAACCIIAABIBCEABAI HisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetTh	285
8 5	MetValIleValThrThrThrThr         :::::           ::::	26
268 2846	luPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn:::    :::::::      ::::::::::::::::::	252 2797
252 2796	tLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnG    :::	235 2769
235 2768	GlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetAlaMe :::   ::::::                 ::::::: GAGTTGGTGCAAATCAAAGGAGAAATAGAAGAAAAT	219 2733
218 2732	heLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp     :::	202 2683
202 2682	uTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPheP	185 2675
185 2674	GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLe:::::::::::::::::::::::::::::::::::	170 2625
169 2624	hrLeuAsnGlyLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGly :::    ::: :::       :::    :::	153 2575
153 2574	uProValLeuTrpArgLysAspGlnHisHisHisArgValGluGlnLeuT:   :::::::::::::::::::::::::::::::::	136 2540
136 2539	IleIlePheAsnLeuLysSerThrPheThrGl::::::::::::::::::::::::::::::::::::	126 2490
125 2489	yrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAsp:::::::    :::::    :::::    :::::    :::::    :::::    :::::    :::::    :::::    ::::::	109 2440
109 2439	nThrSerGluGlyAspLeuAspAspLeuAlaGlnAspLeuLysAspLeuT ::::::::::::::::::::::::::::::::::::	92 2390
92 2389	LeuPheGlnAspLeuAsnGlyGlnSerLeuPheHisGl ::::::   :::        :::::         :::::::	80 2346
79 2345	ASDLeuPheLeuLysSerLeuLysGluTrpAsnTyrPro	67 2317
2316	TTATATGGAGCTACAGCAGAAAGCTGAGTTCTCAGATCAGAAACATCAGA	2267

300	prheileargserheuasphiscysciyaspieu	396
3217	AAAAACTTATTTTACTACAAAGATGTGAAGAAACC	3266
397	aLeuGluGlyValPheSerHisLysPheAspPheGluLeuGl	411
3267	AAATGCATATGAGGATCTTAGTCAAAAATACAAAGCAGCACA	3310
4 (	hrThrGlyLeuLeuC	28
· i	GAAAAGAATTCTAAATTAGAATGCTTGCTAAATGAATGCACTAGTCTTT	3300
428 3361	ysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLys   :::	444 3410
445	heGlnGluTyr	449
3411	AACACCAAGAATTCTTAACAAAATTAGCATTTGCTGAAGAAAGA	3460
4 5	ThrAlaGlyArgArgLeuSerSerLeuL	5
σ	TGATGCTAGAGTTGGAGACAGTGCAGCAGCTCTGAGATCTGAGA	3510
459 3511	euThrSerHisGluProGluGluValThrLysGlyAsnGlyTyrLeuGln::   ::::::::    .     TGACAGATAACCAAAACAATTCTAAGAGCGAGGCTGGTTTAAAGCAA	475 3560
476	ysMetValSerIleSerAspIleThrSerThrTyrSe	488
3561	AAATGCAAAAGGAAGTTAA	3610
4	ThrCysGlySerSerValGluAlaThrArgAlaV :::	
, 🗀	GACTTATTACAAGAGAATGAACAGCTGATGAAGG	0
3646	AIAAIAVAITYTGINHISGIYCYSLEULEUGIYLEU :::	3668
522	ArgProLeuTrpArgGlnGluSerLeuGlnSer	536
3669		3688
537	alLysAsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAsnS	553
3689	TAGGAACTCTGTGAAAGAAAGAGAGAGAGTGAGAAATCAATGTAATT	3738
553	luCysGlyIleHisLeuTyrGlnGluSerThrSerLys	568
3739	TGGATCTTGAAGTTAAAGAAATTTCTCTAGATAGTTAT	3788
56	euSerGlnGluPheGluAlaPhePheGlnGlyLysSerLeuTy	585
20 0	T] bAsnSbrG vAsnT] bDrOAsnTvrTbuDbbAsnDhaDhaCluHisT	0
585	_	602

827 4752	811 .IleValLysSerLeuSerSerGluProCysAspLeuGluGluIleGlnL	
4702	AGAGCTCTTTTAGAACAGACAGGAGATATGTCTCTTTTGAGTAA	
810	809 AspTyr	
808 4652	792 ysMetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMet   ::	
792 4602	781 eLysLeuAlaGluGlyLeuLysAsnLeuLysL :	
781 4552	772AsnIleLysMetAsnGluGluAspAlaIl	
Ü	TGAGCTCTAAAATGTCAGAGCTGCAGACCTATGTTGACTCATTAAAGGCC	
771		
771 4452	759 uGlyAsnLeuLysAsnLeuThrLysLeuIleMetAsp	
759 4402	743 IleHisAspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLe :::    :::    ::::::::::::::::::::::::	
742 4352	732 leThrSerValThrAsnLeuLysThrLeuSer ::::   ::::::::::::::::::::::::::::::	
732 4302	726 eGluaspGluargHisI : :	
726 4252	714 IleTyrSerLeuMetValGluAlaSerProLeuThrIl : : : : : :	
713 4202	697 ysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLysAsn	
697 4152	680 uGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArgC	
680 4102	664 ValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrLe ( :::   ::::::::::   :::    4053 ACAACAATGAACAAGCTGAATGAGCTAGAGAAAATATGTGAAATACTGCA (	
663 4052	648 laValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGlu (	
648 4002	ഹ ⊅	
634 3952	AlaSerTrpGluLysAlaAlaGluAspThrGlyGlyIl 	
617 3908	P H	
3858	GG	

19103-2307

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seq_documentation_block:
   Sequence 2, Application PC/TUS9516216
   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-16216-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5161 AGAAAATGGAAAGTCAAGGGATTATGAAAAATAAGGAAATT...CAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4903 CTGACAGCTCTAGTCTTAGCAGTTTGGGAGACTCCTCCTTTTACAGAGCT 4952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   914
                                                                                               TITLE OF INVENTION: Nucleic Acid Encoding a Transiently TITLE OF INVENTION: Expressed Kinetochore Protein, and I NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         930 ePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901 ysHis.....LeuGluGluValProGlnLeuValLysLeuGly 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  884 uMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuL 901
                                                                                                                                                                                                 APPLICANT: Yen, Timothy J.
APPLICANT: Rattner, Jerome B.
STREET: 1601 MERCETY: Philadelphia
                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuLysGlnLeuValPhe......PheAspPheSerThrLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACCGG......CAGTCCCTCGAGAAGCTAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGAA......GAGCTTGAGTCCCTCTGTGAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                              ACGGAACAACTGTCACTT 5366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGCGTGACTCTGGAGATGGAGTCCAAGTTGGCGGCAGAAAAGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAsp 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGTATTTGTCAGAAAAT.....GAACAGTGGCAACAGAAGCTGA 5298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValLeuS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snArgValSerSerAspGlyTrpLeuAlaPheMetGlyValPheGluAsn 963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGGAGAATCTGACCAGGAAAGAAACCCCTTCGGCCCCAGCGAAGGGT
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                                             E: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                    and Methods
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alignment_block:
US-09-697-089-2 x PCT-US95-16216-2
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Red, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                    2346
                                                                                                                                                                       2440 ATGCCGAATATGAGAGCCTCAGGGATCTGCTAAAATCCAAAGATGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                 2540 GCCTGCCATG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2267 TTATATGGAGCTACAGCAGAAAGCTGAGTTCTCAGATCAGAAACATCAGA 2316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2220 AACGTGTTAGACAGTAAGTCAGTGGAGGTAGAGACCCAGAAA...CTAGC 2266
                                                                                                                                                                                                                109 yrHisThrProSerPheLeuAsnPheTyrProLeuGlyGluAspIleAsp 125
                                      136 uProValLeuTrpArgLysAspGlnHisHisHisArgValGluGlnLeuT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/16216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          IleIlePheAsn.....LeuLysSerThrPheThrGl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eHisMetIleLeuLysLysGlySerGluSerCys.....
                                                                                   CTGGTGACAAATGAAGATCATCAGAGAAGTCTTTTGGCTTTTGATCAGCA
                                                                                                                                                                                                                                                           GTTACTGTCAAATGAAATAATGGACAAAAGACCGGTGTTACCAAGACTTGC 2439
                                                                                                                                                                                                                                                                                                    nThrSerGluGlyAspLeuAspAspLeuAlaGlnAspLeuLysAspLeuT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AsnLeuPheLeuLysSerLeuLysGluTrpAsnTyrPro 79
                                                                                                                                                                                                                                                                                                                                                    ....TCTCAGCTTACTGGGCAAGTTGAAGATCTAGAACACAAGCTTCA 2389
                                                                                                                                                                                                                                                                                                                                                                                        LeuPheGlnAspLeuAsnGlyGln.....SerLeuPheHis......Gl 92
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09-DEC-1995
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48.702
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Percent Identity: 18.426
.CATCATTCCTTTGCAAATATAATTG
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444	ysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePheHisLys	428
3360	GGAAAAGAATTCTAAATTAGAATGCTTGCTAAATGAATGCACTAGTCTTT	3311
428	AspValSerSerValAsnGluAspValLeuLeuThrThrGlyLeuLe	411
411 3310	AlaLeuGluGlyValPheSerHisLysPheAspPheGluLeuGl	397 3267
396 3266	SpPhelleArgSerLeuAspHisCysGlyAspLeu     :::::       ::::      :::   ATCAGTACAAGCAAGAAAACTTATTTACTACAAAGATGTGAAGAAACC	2 8
385 3216	HisLysHisLysGlyValalaAlaSerA	376 3167
375 3166	PheTyrAspLeuLeuIleGlnLysAsnLys :::	366 3117
365 3116	luSerGluPheHisSerHisThrGlnThrThrLeuPheHisThr:::	351 3067
351 3066	UMETLYSThrProLeuPheValValIleThrCysAlaIleGlnMetGlyG	33 <b>4</b> 3029
334 3028	AlaGluGlyLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnLe     ::::   	318 2979
317 2978	luAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLeu :::::	302 2931
302 2930	gHisIleArgGlnPheGlyAlaLeuThrAlaGluValGlyAspMetThrG:::::::::::::   ::::::    cAAGGAAAAAGAGCTGCAACTTTTAAATGATAAGGTA	285 2894
285 2893	HisargPheLysAsnMetVallleValThrThrThrThrGluCysLeuAr:::	269 2847
268 2846	luPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGluAsn ::    :::::   :::::   :::    GTTTTGTGGCTGAAACAAGTCAGCGCATTAGTAAGTTACAGGAAGACACT	252 2797
252 2796	tLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyrAsnG    :::	235 2769
235 2768	GlnLeuLeuAspIleProGlyThrIleArgLySGlnThrPheMetAlaMe :::   :::::           ::::::: GAGTTGGTGCAAATCAAAGGAGAAATAGAAGAAAAT	219 2733
218 2732	heLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCysAsp     :::::::::::::::::::::::::::::::::	202 2683
202 2682	uTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheValPheP 	185 2675
185 2674	GluSerGlyLysGlyLysSerThrLeuLeuGlnArgIleAlaMetLe:::::::::::::::::::::::::::::::::::	. 170 2625
2624	GAGAACAAGGAAGCATGCCTTCAGAGAGGAGTGAATGTCGTTTAGAAGCA	2575

CTTAACAAATTAGCATTTGCTGAAGAAGAAGAATCA CTTAACAAAATTAGCATTTGCTGAAGAAGAAAGAATCA  ThralaGlyargLeuserSerLeul
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4 L D 3	GGAAACTACTAAAT	4202
714 4203	IleTyrSerLeuMetValGluAlaSerProLeuThrIl ::::::::::::::::::::::::::::::::::::	726 4252
726 4253	GluarghisI    :::   aggaggtgaatttggtgaacaaccaaatgaacagcacc	732 4302
732 4303	LysThrLeuSer :::           ::: GAGAGTAATTCCTACGAGCACTTGACA	742 4352
743 4353	uProGlyGlyLeuThrAspSerLe :::     :::::: TTTGCCGAATTGCAAGAGAAATT	759 4402
G	GlyAsnLeuLysAsnLeuThrLysLeuIleMetAsp	
4403	CTTTACAAAGTGAACACAAAATTTTACATGATCAGCACTGTCAGA	4
7		71
Ú.	AGCTCTAAAATGTCAGAGCTGCAGACCTATGTTGACTCATTAAAGGCC	Ü
4503	GGTCTTGTCAACGAATCTGAGAAACTTTCAAGGTGACTTGGT	4552
781 4553	LeuAlaGluGlyLeuLysAsnLeuLysL 	792 4602
792 4603	PheHisLeuThrHisLeuSerAspIleGlyGluGlyMet :::                 :::::        :::::: CCTGACAGCTCTAGTCTTAGCAGTTTGGGAGACTCCTCC	808 4652
809		810
4653 811	TACAGAGCTCTTTTAGAACAGACAGGAGATATGTCTCTTTTGAGTAA eVallysSerLeuSerSerGluProCysAspLeuGluGluIleGlpL	4702 827
_	GAAGGGCTGTTTCAGCAAACCAGTGCAGTGTAGATGAAGTATTTT	7
827 4753	SerâlaAsnâlaValLysIle ::::::::::   ::: TATGTTGACTCATTAAAGGCCGAAAATTTGGTC	839 4802
840 4803	LeuValLysLeuSerIl           GGTGACTTGGTGAAGGAGATGCA	852 4852
852 4853		860
6	GluLySAspGlyAsnGluAla	67
868	sGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLe	884
œ	etLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuL :: .     :::   ::: :::	ō
901	HisLeuGluGluValProGlnLeuValLysLeuGly	913
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SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-947-823-1
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US-09-697-089-2 x US-08-947-823-1
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Percent Similarity:
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                                                                                                                                                                                    17609 TCAAAGAAGATCTCTGCTTTAGATGAGAACATTCCCAAGGACAGAGGT 17658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17248 AAGAAAGATCTCAAACATGTTTATCTGAAAGCCCCAAATTCATCTCAATG 17297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17198 ACCAAACAAATTGTGCAACCCTAGACTTGCTGGAAAATATTGAACTCCTC 17247
                                                                             17659 CTAATCGTTGTGAACTCT..........CCCAAGAAACCAGTTGA 17693
                                                                                                                                                                                                                                                                                             17559 CTTACATCTTATTTTCTCACTTCCCATTACCATAAAGAAGATCAAACTTA 17608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17368 TCTAATGCTTATTCAATTTCTTTGATAAAGGAAATCGAGTTGGTGAG 17417
                                                                                                                                                                                                                                                                                                                                                                                                    17509 TATGAGGCAAAAGATGTCATAGATTCAATTATTGTTCGAGATAATGGTCT 17558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17298 TIGCTICCCCATGAGIGATGGACCACTCTTCATGCATCTT....... 17337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17148 GACTCTTGTACGTGACTTGGAAGAGAAATTAAGGAATAAAGAGGGTAATA 17197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17107 GATCTCTTGGCTCATGTT......GGAACACTTACCAGGGAGGTATC 17147
442 eHisLysSerPheGlnGluTyrThrAlaGlyArgArgLeuSerSerLeuL 459 :::|||||||:::
                                                                                                                               426 LeuLeuCysLysTyrThrAlaGlnArgPheLysProLysTyrLysPhePh 442
                                                                                                                                                                                                                                         409 luLeuGlnAspValSerSerValAsnGluAspValLeuLeuThrThrGly 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 HisThrPheTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGl 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 leGlnMetGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPhe 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 IleLysGluLeuAlaGluGlyLeuLeuLeuGlnIleGlnLysSerArgCy 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 ......GluValLeu 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 GluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValG1 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 yAspMetThrGluAspSerAlaGlnAlaLeuIleArg...... 310
                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGAGCAAGGATTGTATAAAGATATCTGGGCACGTGTTCTAGATGTGGCT 17508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....CTACACATGCACTTAAATGATTTGCTAGAT 17367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLeuArgAsnLeuMetLysThrProLeuPheValValIleThrCysAlaI 347
                                                                                                                                                                                                                                                                                                                                          .....HisLysPheAspPheG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 144.50
: 0.335
: 46.047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 936
Gaps: 51
Percent Identity: 19.765
```

18568	AGGATTTGTG	18519
658	LysGlnG	656
00	CATGOTTGCTTCACTTTGCAAGTTGGCCGAAGGACACTCCTTTGACAA	18469
655	PhePheAsnTrp	652
18468	EU	651 18419
18418	TGAAGTTCAAAGTAGTTTGAGTTCTTTTATTTTGAACAGTGAAGTGGAAG	18369
	eHisMetGluGluAlaProGluThrTyrIleProSerArgAlaValSerL	634
634 18368	GlyGlyAlaMetAlaSerTrpGluLySAlaAlaGluAspThrGlyGlyIl::::   :::   :::   :::   :::    :::    :::	618 18325
617 18324	isLeuProAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr::::::::::::::::::::::::::::::::::::	601 18278
601 18277	GlyAsnIleProAspTyrLeuPheAspPhePheGluH	589 18228
18227	AGACCAGATGAAAG	18178
588		588
588 18177	heGluAlaPhePheGlnGlyLysSerLeuTyrIleAsnSer	575 18137
575 18136	SerLysSerAlaLeuSerGlnGluP     ::      :::    TTTTCCTGAAGCTAAGAAAGGAAGTAGGATTATTTTGACAACTCGAGAAA	567 18087
566 18086	nSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThr	18038
552 18037	bysAsnThrThrGluGlnGluIleLeuLysAlaIleAsnIleAs :::         :::        TGCGGAAACAACTGTTTGGAAAGAGGTATCTTATTG	538 18002
537 18001	erVal	536 17952
536 17951	erIleAlaLysArgProLeuTrpArgGlnGluSerLeuGlnS :::::::	519 17902
519 17901	rgAlaValMetLysHis.LeuAlaAlaValTyrGlnHisGlyCysLeuLe::::    :::          :::              ::: AGTCAGTTTCTAGACATTTTGACCTTCGTGCATGGTGCACGGTC	503 17858
503 17857	TTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrA : :::::	486 17820
486 17819	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh     :::	470 17773
469 17772	euThrSerHisGluProGlu	459 17723
17722	ACAACTGATAAAATAA	17694

008		674
8569	AGATGAAGGGTATAGAAGAAGTGGTGAAG	18597
675 .8598	GlnAspIleThrTyrLeuGlyLysIlePheSerSerAlaThrSerLeuAr	691 18636
691	leLysArgCysAlaGlyValAlaGlySerLeu     :::      :::::	704
8637	TGTTTCAATGAGATAGGTGATATACTGAATTTCC	18670
705 8671	euValleuSerThrCysLys 	712 18720
13	:	723
17/R	TGATCGGATAAGATCAAGTGCTCCATCAGATTTGTTGCCTCG	18770
724 8771	TTAATT	731 18820
732	IleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGln	47
8821	::: GTCATGTTCGATTCAAATAAGAAAAGGCATTCTGGTAAACACCTCTAT	18870
748	AsnGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLy	763
763	.snLeuThrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspA	780
8921	ACACTTGAGGCTTATTAGAGTGTTGGACCTGGAACCCTCTT	18970
8971	LalleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPhe         ::: :::       :::::       :::::       :::::         :::::	796 19014
797 9015	HisLeuThrHisLeuSerAspIleGlyGluGlyMetAspTyrIleVa	812 19061
812 9062	llysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuValS	829 19105
829 9106	erCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis	845 19146
846 9147	AsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGl::::	861 19196
861 9197	uLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValL::   :::   :::    ::::   :    :::::   ::::  TATGGATGCAGATGAATCAATATTGATAGCAAAGGACACAAAGT	878 19240
878 9241	euGluGlnLeuThrAlaLeuMetLeuProTrpGlyCysAsp	891 19290
892 9291	uSerSerLeuLeuLysHisLeuGluGluValProGl :::::::         ::::::	908 19325
90E	nLeuValLysLeuGlyLeuLysAsnTrpArg	918

	CE CHARACTERISTICS:
	TELEFAX: (415) 576-03
	; TELECOMMUNICATION INFORMATION:
	REFERENCE/DOCKET NUMBER: 0
	<b>-</b>
	INFORMATION
	ION DATA:
	; APPLICATION NUMBER: PCT/US97/18802 ; FILING DATE: 09-OCT-1997
	ION DATA:
	; FILING DATE: 09-0CT-199/ CLASSIFICATION: 800
	CATION NUMBER
	-
	PERATING SYSTEM: PC-DOS/MS-DOS
	; COMPUTER: IBM PC compatible
	ER READABLE FORM:
	STATE:
	CITY: San Francisco
	ADDRESSEE: Townsend and Townsend and Crew I
	ESPONDENCE ADDRESS:
	TITLE OF INVENTION: Pest Resistance in Plants
nferring	TITLE OF INVENTION: Procedur
	APPLICANT: Bodeau, John
	APPLICANI: NaiOshian, isgoun
	APPLICANT: Williamson,
	RAL INF
	documentation_ quence 2, Appl
່ວ	<pre>seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-947-823-</pre>
	19640 AAGAC 19644
	1010 spAsp 1011
3G 19639	19599 TGATACAATCATCCAGGGAGAAGAATGGAACATGGGGGAGG
1010	993 sLeuThrPheLeuGlnGluAlaArgLeuValGly
TA 19598	19549 TCACTATCAACAATAGCGAGACTGCCCAACCTTGAAAATTTGTCCCTTTA
Ly 993	Ser
	AAATTTGAAAGAACTGTTGTTGTATGACTTTCCTCTGACATCCG
È	6
CC 19498	19452 CTGTGGGTCCTCTGTTGCGACAAATCGGCCGTGGGATTTTCACTTCC
1P 961	yTrpLeuAlaPheMetGlyVa 
CA 19451	TTTAAAAGTTCAA
Le 944	928 GlyAlaphePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLe
TA 19425	
eu 927 ::	919LeuThrAspThrGluIleArgIleLeu

```
; NAME/KEY: CDS; LOCATION: 85..3852; OTHER INFORMATION: /note- "Copy 1 cDNA for M1 nematode; OTHER INFORMATION: resistance gene of tomato" US-08-947-823-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-697-089-2 x US-08-947-823-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 144.00
Ratio: 0.292
Percent Similarity: 41.255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ign seg 1/1 to: US-08-947-823-2 from: 1 to:
                                                                                                          1184 TCAAACATGTTTATCTGAAAGCCCTGGATTCATCTCAATGTTGCTTCCCC 1233
                                                                                                                                                                                                                                                                                                         1155 GGAAAATATTGAA.......CTCCTCAAGAAAGATC 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1105 AGGAATAAAGAGGGTAATAACCAAACAAATTGTGCAACCCTAGACTTGCT 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1005
                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1055 TACTTACCAGGGAGGTATCAACTCTTGTACGTGACTTGGAAGAGGAACCA 1104
154 .....LeuAsnGl 156
                                                                                                                                                                                                    144 lnHisHisArgValGluGlnLeuThr.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              855 GCTTCTAGAAACCTCTCCAGATATTCTGAGGGAATATCTAATTCCTCTGC 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||:::||| |||::: || || ||::: || ||::: |||::: |||::: |||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:: ||:: ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :::::||||||
755 TACTCTTGAAGATCGTTCCGGTTGAACTGGAGGTTATACACATATGTTAT 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     705 TGAGGATGAACAAAATGATAGAGACTCTCGACTTTTCAAGCTAGCACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              905 AAGAGCACATGGTAACTGTTATTACCCCTAGCACTTCAGGGGCTCGAAAC 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          655 TTCCTTTGGGATGATCAGACTGATGAAGACTCTCGACTCTCCGAGCTAGA 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 PheHisGlnThrSerGluGlyAspLeuAspAspLeuAlaGlnAspLeuLy 106 :::||| || |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 heGlnAspLeu.....AsnGlyGlnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 etIleLeuLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 PheValTrpAsnValLeuAsnArgGluGluValAsnIleIleCysCysGl 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3997 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                        ePheAsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspG 144 : |||| :::|||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....LysGlySerGluSerCys.....AsnLeuPheLeuLysSe 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....Pro 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTCATGTCATGATGGAATTCCTATTACTTATTCTTTCTGATATGCCCAA 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACTTTATTCATCATGACAAACTTTTTGATCTCTTGGATCGTGTCGGAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 1195
Gaps: 56
Percent Identity: 18.075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3997
                                                                                                                                                                                                              153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
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```

<u> </u>	1234	ATGAGTGATGGACCACTCTTCATGCATCTTCTACACATACACTTAAATGA	1283
<u>.</u>	156	yLeuLeuGlnAlaLeuGlnSerProCysIleIleGluGlyGluSerG 1       ::::::	72
		lyLysSerThrLeuLeuGlnArgIleAlaMetLeuTrpGlySer	88
H	.334	AGCTGGTGAAGCAAGACCTG	353
125	189	GlyLysCysLysAlaLeuThrLysPheLysPheValPhePheLeuArgLe 2              :::	377
ν.	205	lnGly	222
. :		rgagcaaggattgtataaagatctctgggcacgtgttctag	ء د
<u> </u>	1424	ATGTGGCTTATGAGGCAAAAGATGTCATAGATTCAATTATTGTTCGAGAT 1	473
	224	ProGlyThrIleArgLySGl 2	30
14	174	TCAC	521
15	522	nThrPheMetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuL 2 :::       :::       ATCAPACTTATCAPAGAAGAGATCTCTGCTT 1	.552
15	247	euAspGlyTyrAsnGluPheLysProGlnAsnCysProGluIleGluAla 2        :::        ::: ::::: TAGATGAGAACATTCCCAAGGACAGAGGT 1	.581
15	64 82	LeuIleLysGluAsnHisArgPheLysAsnMetValIleValThrThrTh 2	631
Ε	280 1632	rThrGluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluV 2           ::: ::	97
=	297 1649	alGlyAspMetThrGluAspSerAlaGlnAlaLeuIleArgGluValLeu 3	677
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ا د		מאלי ל
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694 2707	682 sILePheSerSeralaThrSerLeuArgLeuGlnIle	

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CURRENT APPLICATION NUMBER: US/09/180,439
CURRENT FILING DATE: 1998-12-06
EARLIER APPLICATION NUMBER: PCT/GB97/01249
EARLIER FILING DATE: 1997-05-08
EARLIER APPLICATION NUMBER: GB 9609681.3
EARLIER APPLICATION NUMBER: GB 9619924.5
EARLIER APPLICATION NUMBER: GB 9619924.5
INUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 3541
TYPE: DNA
ORGANISM: Lycopersicon esculentum
US-09-180-439-5
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APPLICANT: Dixon, Mark S
APPLICANT: Hatzivanthis, Kostas
APPLICANT: Jones, David A
APPLICANT: Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
FILE REFERENCE: 620 - 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
Sequence 5, Application US/09180439
Patent No. 6225532
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1356 TCTGGCTCTATTCCTGAAGAA......ATAGGTTACCTAAG 1390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3390 GACAAATCGGCCGTGGGATTTTCACTTCCCTTCAAATTTGAAAATACTG. 3438
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                                                    725
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                                                                                                                                                                                                                                                                                                                                       950 rSerAspGlyTrp...LeuAlaPheMetGlyValPheGluAsnLeuLysG 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                928 lyAlaPhePheGlyLysAsnPro...... 935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....LeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSe 950
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850 1828	ASNAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLe	835 1779
834 1778	erCysCysLeuserala        	829 1729
829 1728	uGluIleGlnLeu :::::::    ATCACTAGAACTG	823 1679
823 1678	GlyMetAspTyrIleValLysSerLeuSerSerGluProCysAspLeuGl::::::::::::::::::::::::::::::::::::	807 1629
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805 1578	nLeuLysLysMetCysLeuPheF    :::::::::  CTTGAGTTCTCTTACTAATCTAI	789 1529
789 1528	IleLysMetAsnGluGluAspAlaIleLysLeuAlaGluGlyLeuLysAs ::::::::     ::: AATCAGCTTTCTGGCTCTATTCCTGAAGAAATAGGTTA	773 1491
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us-09-697-089-2 x us-08-947-823-4
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-947-823-4
                                                                                                                                               Ratio:
Percent Similarity:
                                         Align seg 1/1 to: US-08-947-823-4 from: 1 to: 3982
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY_AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-070210US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08947823 Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2261 GAAAGGGATGAGGACAGTTGATAAAACAATGGAGGAA 2297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
282 GluCysLeuArgHisIleArgGlnPheGlyAlaLeuThrAlaGluValGl 298
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3982 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Procedures and Materials for Conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Milligan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               964 uLysGlnLeuValPhePheAspPheSerThrLysGlu 976
                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 87..3860
OTHER INFORMATION: ,
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kaloshian, Isgouhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
DLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williamson, Valerie M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bodeau, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415)
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0.333
46.047
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                                                                                                                                                                                                                                                                                         /note= "Copy 2 cDNA for M1 nematode
resistance gene of tomato"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
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Gaps: 50
Percent Identity: 19.444
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,		1
704	sAlaGlyValAlaGlySerL	691
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4 7	eGluAsnLeuLysGlnLeuValPhePheAspPheSerThrLysG :::        :::  :::        TCAAATTTGAAAGAACTGTTGTTGTATGACTTTCCTCTGACATCCG	ו א פֿ
961 3428	uAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyValP ::::::::::::::::::::::::::::::::::::	944 3383
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891 3218	euGluGlnLeuThrAlaLeuMetLeuProTrpGlyCysAsp      :::   	878 3169
878 3168	uLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValL :    :::::   :::::  TATGGATGCAGATGAATCAATATTGATAGCAAAGGACACAAAGT	861 3125
861 3124	LLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGl         :::   ::::::  AAGTTGCGAGTGCTGTCCGTGGGTGCTTCTTTCTTTGA	846 3075
845 3074	erCysCysLeuSerAlaAsnAlaValLysIleLeuAlaGlnAsnLeuHis	829 3034
829 3033	llysSerLeuSerSerGluProCysAspLeuGluGluIleGlnLeuValS    :::   :::  TTTCTCTTTCTCAAACCTCTGGAATCTAGAAAGTCTGTTTGTGT	812 2990
812 2989	HisLeuThrHisLeuSeraspIleGlyGluGlyMetAspTyrIleVa 	797 2943
796 2942	laIleLysLeuAlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPhe	780 2899
780 2898	SASNLeuThrLySLeuIleMetAspAsnIleLySMetAsnGluGluAspA :::             ::	763 2849
763 2848	ASNGlnArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLy :::    :::	748 2799
747 2798	IleThrSerValThrAsnLeuLysThrLeuSerIleHisAspLeuGln  !!!	732 2749
731 2748	LeuThrIleGluAspGluArgHis	724 2699

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alignment_block:
US-09-697-089-2 x US-08-514-014-3
                                                                                                                                                                                                                                           alignment_scores:
Quality: 142.00
Ratio: 0.553
Percent Similarity: 47.156
                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 52..2034
US-08-514-014-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-514-014-3
                                                                                                                                      Align seg 1/1 to: US-08-514-014-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08514014 Patent No. 5707829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: McCleher, Kerry
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: BNCODED THEREBY
TITLE OF INVENTION: ENCODED THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2IF: ULLIU COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1010 spAsp 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3527 TGATACAATCATCCAGGGAGAAGAA.....TGGAACATGGGGGAGG 3567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3568 AAGAC 3572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                          265 ACCTTCAGCAGACTCATGAATCTTACC.....TTTTTTGGATTTAAC 305
                                                                        486 ThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaTh 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2582 base pairs
TYPE: nucleic acid
502 rArgAlaValMetLys.....HisLeuAlaAlaValTyrGlnHisGlyC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           993 sLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAspA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSE: Genetics Institute, Inc. -- Legal Affairs
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 87 Cambi
CITY: Cambridge
STATE: Massachus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 02140
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : cDNA
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                                                                                                                                                                                                                                               Length: 545
Gaps: 24
Percent Identity: 22.936
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                                                                                                                                        from: 1
                                                                                                                                      to: 2582
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LeuT 756	39 sThrLeuSerlleHisAspLeuGlnAsnGlnArgLeuProGlyGly	
CeuLy 739 :::   STGAA 1121	23 ProLeuThrIleGluAspGluArgHisIleThrSerValThrAsni	72 107
laSer 722      CAGT 1071	6 euValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAl            ::::::::::::::::::::::::::	70 102
SerL 706 :::  SAAAT 1027	05	70 97
<b>A</b>	28 ACATTTCAGTGCTTCACCCAACTCCAAGAATTGGATCTGACAG	
704	04 Leu	70
LySer 703 ::::: CACC 927	87 laThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValalaGly::::::::::::::::::::::::::::::::	
SerA 687	73 nLysGlnAspIleThr : ::      ::: 28 TGACGAAGATATTAGTTCAGCCAT	
LeuAs 673 ::::: :ATTGA 827	7 GlnGluPheArgThrLeuGluValThrLeuArgAspPheSerLys	
pLys 656 From 777	46 erArgAlaValSerLeuPhePheAsnTrpLys	
ePros 646 CCAAA 727	29 uAspThrGlyGlyIleHisMetGluGluAlaProGluThrTyrIl :::::::      ::::: 78 TAATGTTAAAGGTATTGAGCTTGGGGCTTTTGATTCAACGGTCTT	62 67
AlaG1 629 ::::: GGCAA 677	21 MetAlaSerTrpGluLysAla	62 62
620 AAGAC 627	12 leLysLeuAspPheTyrGlyGlyAla	
PheI 612 :::: PCTGA 577	95 uPheAspPhePheGluHisLeuProAsnCysAlaSerAlaLeuAspPl 	
TyrLe 595 CATTAA 545	79 PheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp: ::: ::        :::::   ::::    ::: GAAAACTTGGAAGCTTGTATCTTGGAAGCAACCATATTTCCTC	57 49
AlaPhe 578 ::: AATCTG 495	65 erThrSerLysSerAlaLeuSerGlnGluPheGlu ::   :::	4 5 4 5
GlnGluS 565 TTAATCC 451	48 alleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyr       ::: 36CATCTTTTC	43
euLysal 548        GAAG 435	2 GluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLe        :::::    :::   ACATCGCTTAATGGGCCCAAGTCA	40
rgGln 531 ::: CAGAA 405	17 ysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpAr     :::::: :::       56 AATTAAGCACACTTGTGTTAACTGGAAATCCCCTGATATTCATGGC	51 35
CATC 355	::: ::::::      106 TAGGTGCCAGATTAACTGGATACATGAAGACACTTTTCAAAGCCAT	30

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08833823 Patent No. 5969093
                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICANT: McCoy, John
APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1565 CTTGT.....GGTCTCCTCTATAGACCAGCAAGCATTCCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              922 rGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                874 gMetAsnValLeuGluGlnLeuThrAlaLeu....MetLeuProTrpG 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     858 AsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspAr 874
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COUNTRY:
                                                         CITY: Cambridge
                                                                                  STREET:
                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGTCCCACTTGCAAACCTTAAACCTGAGCCACAATGAGCCTCTTGGT 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACCAACCTACTTCAGACCGTGGGCAGCTTGGAGGTTCTGATTTTGTCCT 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....LeuAspLeuSerGlu......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heGlnGlnLeuAsnLeuAlaGlyAsnArgValSer
                      Massachusetts
                                                                               E: Genetics Institute, Inc.
87 CambridgePark Drive
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                                                                                                                  Legal Affairs
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alignment_block:
US-09-697-089-2 x US-08-833-823-3
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; LOCATION:
US-08-833-823-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-833-823-3 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                            517 ysLeuLeuGlyLeuSerIleAlaLysArgProLeu.....TrpArgGln 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 rArgAlaValMetLys.....HisLeuAlaAlaValTyrGlnHisGlyC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 ThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                              532 GluSerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAl 548
                                                                                                                                                                                                                                                                                                                                                                                           356 AATTAAGCACACTTGTGTTAACTGGAAATCCCCTGATATTCATGGCAGAA 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 TAGGTGCCAGATTAACTGGATACATGAAGACACTTTTCAAAGCCATCATC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CI
                                              496 GAAAACTTGGAAAGCTTGTATCTTGGAAGCAACCATATTTCCTCCATTAA 545
                                                                      579 PheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAspTyrLe 595
                                                                                                                                452 AAACGGGAATATCCAATCTC.....GAGTTTATTCCAGTGCACAATCTG 495
                                                                                                                                                                      565 erThrSerLysSerAlaLeuSerGlnGluPhe.......GluAlaPhe
                                                                                                                                                                                                                436 .....CATCTTTCTTAATCC
                                                                                                                                                                                                                                                            548 aIleAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluS
                                                                                                                                                                                                                                                                                                      406 ACATCGCTTAATGGGCCCAAGTCA..........CTGAAG.. 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 ACCTTCAGCAGACTCATGAATCTTACC.....TTTTTGGATTTAAC
595 uPheAspPhePheGluHisLeuProAsnCysAlaSerAlaLeuAspPheI 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
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DEDNESS: double
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52..2034
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47.156
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852	SIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuSerIle	838
838 1364	YSCYSLeuSerAlaAsnAlaValLy            ::  CCCGCTTACACATTAATGCTCCACA	822 315
821 1314	pTyrIleValLysSerLeuSerSerGluProCysAsp :::::    :::     :::     :::CTCCAGAGTCAGGCATTCAAAGAATGTCCTCAG	806 .282
806 1281	SerAspIleGlyG  ::: ::     GAGCCTCTTGGT.	789 .233
789 1232	luGlyLeuLysAs          CTCAAAAA	773 .189
772 1188	hraspSerLeuGlyasnLeuLysasnLeuThrLysLeuIleMetaspAsn ::::::            :::::   TGGAGAAACTAGGAAACCTTCAGACACTTGATTTAAGCCAT	756  148
756 1147	. >	739 1122
739 1121	ProLeuThrIleGluAspGluArgHisIleThrSerValThrAsnLeuLy :::::             :::               :::	723 [072
722 1071	euValLeuSerThrCysLysAsnIleTyrSerLeuMetValGluAlaSer             ::	706   028
706 1027	CTTGAAAGGGTTACCCTCTGGGATGAAGGGTCTGAACTTGCTCAAGAAAT	705 978
977	TCAGTGCTTCACCCAACTCCAAGAATTGGATCTGACAGCAACTCA	928
704		704
703 927	laThrSerLeuArgLeuGlnIleLysArgCysAlaGlyValAlaGlySer::::::::::::::::::::::::::::::::::::	687 878
687 877	nLysGlnAspIleThrTyrLeuGlyLysIlePheSerSerA : ::     ::         GACGAAGATATTAGTTCAGCCATGCTCAAGGGACTCTGTGAAATGTCTG	673 828
673 827	gThrLeuGluValThrLeuArgAspPheSerLysLeuAs 	657 778
656 777	ArgAlaValSerLeuPhePheAsnTrpLys :::   :::::      TIGGAGGAACTCCAAATTGTCTGTTATATTCAATGGTCTG	646 728
646 727	llyGlyIleHisMetGluGluAlaProGluThrTyrIleProS        :::::  All  :::::    AAGGTATTGAGCTTGGGGCTTTTGATTCAACGGTCTTCCAAA	629 678
629 677	MetAlaSerTrpGluLysAlaAlaGl 	621 628
620 627	YrGlyGlyAla	612 578
577	:	546

	ATCTACCTCAATCTGGCTGCCAACAGCATTAAC 1719	1687
	heGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 950	939
1686	CAGCATTGATTCTCTTAGCCATCTTAAGGGA	1656
939	rGluIleArgIleLeuGlyAlaPhePheGlyLysAsnProLeuLysAsnP	922
1655	1606 TTGGGAAAATGAGCCATGTAGACTTAAGCCACAACAGCCTGACATGCGA 1655	1606
922	ValProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspTh 922	906
1605	CTTGTGGTCTCCTCTCTATAGACCAGCAAGCATTCCACAGC 1605	1565
905	lyCysAspValGlnGlySerLeuSerSerLeuLeuLysHisLeuGluGlu	889
1564	1515 GACCAACCTACTTCAGACCGTGGGCAGCTTGGAGGTTCTGATTTTGTCCT 1564	1515
889	gMetAsnValLeuGluGlnLeuThrAlaLeuMetLeuProTrpG	874
1514	CGCCATCTCAACTTAAAAAGGGAATCACTTTCAAGATGGGACTATCACGAA 1514	1465
874	AsnTyrLeuGluLysAspGlyAsnGluAlaLeuHisGluLeuIleAspAr	858
1464	GCTTCCTTGATACCAGCAATCAGCATCTTCTAGCAGGCCTACCAGTTCTC 1464	1415
857	LeuAspLeuSerGlu	853
1414	1365 AAGTCCCTTCCAAAACCTCCATTTCCTTCAGGTTCTGAATCTCACTTACT 1414	1365

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| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AAS33946 + 5 |
| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AAA339384 + 5 |
| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AAA39988 + 5 |
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| SIDSZ/gcgdata/geneseq/geneseqn/NA1999_DAT: AAX398001 + 5 |
| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AA171263 + 5 |
| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AA171264 + 5 |
| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AA171264 + 5 |
| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AA171264 + 5 |
| SIDSZ/gcgdata/geneseq/geneseqn/NA2001_DAT: AA17129000 + 5 |
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Natabase sequences: 930621
Atabase length: 428662619
Search time (sec): 126.370000
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-Q-/cgn2_1/USPTO_spool/US09697089/runat_25032002_105138_11194/app_query.fasta_1.1097
-Q-/cgn2_1/USPTO_spool/US09697089/runat_25032002_105138_11194/app_query.fasta_1.1097
-DB-N_Geneseq_1101 -QFMT-fastap -SUFFIX-rng -GAPOP-12.000
-GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct
-THR_MAX-100 -THR_MIN-0 -ALIGN=15 -MODE-LOCAL -OUTFNT-pfs
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09697089_eCGN1_1_290 -NCPU-6 -ICPU-3 -LONGLOG
-NORM-10 -MAXLEN-20000000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway; cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia; myocardial infarction; inflammatory disorder; coronn's disease; insulin-dependent diabetes; contact dermatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis; ischaemic brain injury; hypoxic brain injury; ss; kidney ischaemia; reperfusion injury; acute bacterial meningiti excitotoxic brain damage; liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human caspase recruitment domain 12 (CARD-12) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200130971-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psoriasis; graft rejection; bacterial infection; lepromatous leprosy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS03945 standard; cDNA; 3133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 36..3110
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Human CARD-12"
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Isolated caspase recruitment domain-12 polypeptide and nucleic acids encoding them, useful for treating and diagnosing disorders associated with abnormal apoptosis such as cancer, arthritis and Alzheimer's

P-PSDB;

2001-308628/32. DB; AAU02880.

27-OCT-1999;

99US-0161822

(MILL-) MILLENNIUM PHARM INC

J,

Robison

26-OCT-2000; 2000WO-US29643

Claim 2; Fig 1; 93pp; English

The sequence represents a cDNA which encodes the human caspase recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a number of proteins that transmit signals that activate apoptosis and inflammatory pathways in response to stress and other stimuli. Therefore CARD-12 and its corresponding nucleic acid may be used in treatment and diagnosis of patients suffering from disorders associated with an abnormal level (an increase or a decrease) of apoptotic cell death or abnormal activity of stress-related pathways. The disorders include cancer, viral infections (e.g. caused by poxviruses, adenoviruses), autoimmune disorders (e.g. systemic lupus erythematosis, arthritis), neurological disorders (e.g. Alzheimer's disease, amountophic lateral infarction, stroke), inflamm Crohn's disease, insulin-dep psoriasis, graft rejection), sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial stroke), inflammatory and immune system disorders (e.g. ease, insulin-dependent diabetes, contact dermatitis, graft rejection), bacterial infections (e.g. tuberculosis leprosy), Therefore, Ø

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Quality: 5281.00
Ratio: 5.157
Percent Similarity: 100.000
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US-09-697-089-2 x AAS03945
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                                   217 sAspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetA 234
                                                                                  201 PhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrLeuCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is chaemia/reperfusion\ injury,\ excitotoxic\ brain\ damage,\ acute\ bacterial\ meningitis\ and\ liver\ disease.
234 laMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAspGlyTyr
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                       TGATCAACTCCTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGG
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1635	6 CCTTCTCGGACTTTCCATCGCCAAGAGGCCTCTCTGGAGACAGGAATCTT	158
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1585		153
500	4 hrserThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu	48.
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484	7 lThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleT	46
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467 1435	1 AlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluVa 	<b>4</b> 5
450	4 rgPheLysProLysTyrLysPhePheHisLysSerPheGlnGluTyrThr	43
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334 1035	7 uAlaGluGlyLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnL 	31 <sup>.</sup>
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935		88
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885		83
267 835	1 AsnGluPheLysProGlnAsnCysProGluIleGluAlaLeuIleLysGl	25 78
785	6 CCATGCTGCTGAAGCTGCGGCAGAGGGTTCTTTTCCTTGTTGATGGCTAC	73

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Human; sheep; pig; co
KW Human; sheep; forensic
KW diagnostics; forensic
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PN W25-JAN-2001; 2001W0-U
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PR 17-JUL-2000; 2000US-0
PR 03-AUG-2000; 2000US-0
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biodiversity; gene therapy; nutrition; ss
                                                                                                                                                                             Human; sheep; pig; cow; fruit fly; yeast; tomato; monkey; dog; sea urchin; expressed diagnostics; forensic test; gene mapping;
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|TGCTTTTAAACTAGTAACTGCT
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; 2000US-0617746.
; 2000US-0631451.
; 2000US-0663870.
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967 3131	SerAspGlyTrpLeuAlaPheMetGlyValPheGluAsnLeuLySGlnLe	951 3082		
950 3081	SnProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer 	934 3032		
934 3031	pargLeuThraspThrGluIleArgIleLeuGlyalaPhePheGlyLysA  gagaCTCACAGATACAGAGATTAGAATTTTAGGTGCATTTTTTGGAAAGA	917 2982		
917 2981	LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTr 	901 2932		
900 2931	euMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 	884 2882		
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834 2731	rGluProCyśAspLeuGluGluIleGlnLeuValSerCysCysLeuSerA 	817 2682		
817 2681	LeuSerAspI1eG1yG1uG1yMetAspTyrI1eVa1LysSerLeuSerSe 	801 2632		
800 2631	laGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis 	784 2582		
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents a genomic DNA which encodes the human caspase recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in number of proteins that transmit signals that activate apoptosis and inflammatory pathways in response to stress and other stimuli. Therefore CARD-12 and its corresponding nucleic acid may be used in treatment and diagnosis of patients suffering from disorders associated with an abnormal level (an increase or a decrease) of apoptotic cell death or abnormal activity of stress-related pathways. The disorders include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia; myocardial infarction; inflammatory disorder; crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leprosy; tuberculosis; ischaemic brain injury; hypoxic brain injury; ds; kidney ischaemia; reperfusion injury; acute bacterial meningitis; excitotoxic brain damage; liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated caspase recruitment domain-12 polypeptide and nucleic acids encoding them, useful for treating and diagnosing disorders associated with abnormal apoptosis such as cancer, arthritis and Alzheimer's
                                                                                                                                                                                                                                                                                          Sequence
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                                                                                             Similarity:
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                                              MetAlaMetLeuLeuLysLeuArgGlnArgValLeuPheLeuLeuAspGl
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                                                                                                ATGGCCATGCTGCAAGCTGCGGCAGAGGGTTCTTTCCTTCTTGATGG
                                                                                                                                               TCTGTGATCAACTCCTGGATATACCTGGCACAATCAGGAAGCAGACATTC
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                                                                                                                                                                                                            eValPhePheLeuArgLeuSerArgAlaGlnGlyGlyLeuPheGluThrL
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582 2217	hrSerLysSerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLys	566 2168
566	eAsnIleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerT	549
2167		2118
549	SerLeuGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAlaII	533
2117		2068
532	5 1yCysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGlu	516
2067		2018
516	3 IGlualaThrargalaValMetLysHisLeuAlaAlaValTyrGlnHisG	499
2017		1968
499	3 IleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerVa	483
1967		1918
482	5 luValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAsp	466
1917		1868
466 1867	TThralaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluG	449 1818
449	3 GlnargPheLysProLysTyrLysPhePheHisLysSerPheGlnGluTy	433
1817		1768
432	5 alasnGluAspValLeuLeuThrThrGlyLeuLeuCysLysTyrThrAla	416
1767		1718
416 1717	UG1yVa1PheSerHisLysPheAspPheGluLeuGlnAspVa1SerSerV	399 1668
399	3 AlaSerAspPhelleArgSerLeuAspHisGysGlyAspLeuAlaLeuGl	383
1667		1618
382	5 heTyrAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAla	366
1617		1568
366	3 tGlyGluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrP	349
1567		1518
349	3 AsnLeuMetLysThrProLeuPheValValIleThrCysAlaIleGlnMe	333
1517		1468
332	5 luLeuAlaGluGlyLeuLeuLeuGlnIleGlnLysSerArgCysLeuArg	316
1467		1418
316	P pMetThrGluAspSeralaGlnAlaLeuIleArgGluValLeuIleLysG	299
1417		1368
299	3 CysLeuArgH1s11eArgG1nPheG1yA1aLeuThrA1aG1uVa1G1yAs	283
1367		1318

ysalaSerālaLeuāspPheIleLysLeuāsp gT[	AGCTCTTCATGAACTG	66 luAlaLeuHisGluLeu	849 sLeuSerIleLeuAspL                  3018 ACTGAGCATTCTTGATT	833 SerAlaAsnAlaValLy                   1	816 erSerGluProCysAsp                 2918 CAAGTGAACCCTGTGAC	799 rHisLeuSerAspIleG                     2868 CCACTTGTCTGACATTG	783 LeuAlaGluGlyLeuLys                   2818 CTAGCTGAAGGCCTGAAA	766 hrLysLeuIleMetAsp 	749 nArgLeuProGlyGlyL                2718 ACGGCTGCCGGTGGTC	733 ThrSerValThrAsnLe                    1	716 erLeumetvalGluAla               2618 CTCTCATGGTGGAAGCC	699 yValAlaGlySerLeuS                   1568 TGTGGCTGGAAGCCTCA	683 IlePheSerSerAlaTh                  2518 ATATTCAGCTCTGCCAC	666 euargaspPheSerLys 	649 ISerLeuPhePheAsnT                 2418 ATCTTTGTTCTTCAACT	633 GlyIleHisMetGluGl                   2368 GGAATCCACATGGAAGA	616 heTyrGlyGlyAlaMet                  2318 TTTATGGGGAGCTATG	599 eGluHisLeuProAsnC               2268 TGAACATTTGCCCAATT	ZZIO AGCTTATATATCAACTC
	ATCGACAGGATGAACGTGCTAGAACAGCTCACC pGlyCysAspValGlnGlySerLeuSerSerLe	IleAspArgMetAsnValLeuGluGlnLeuThr	erGluAsnTyrLeuGluLysAspGlyAsnG                      CAGAAAATTACCTGGAAAAAGATGGAAATG	SIleLeuAlaGlnAsnLeuHisAsnLeuValLy 	LeuGluGluIleGlnLeuValSerCysCysLeu 	lyGluGlyMetAspTyrIleValLysSerLeuS 	AsnLeuLysLysMetCysLeuPheHisLeuT 	AsnīleLysMetAsnGluGluAspAlaīleLy 	euThrAspSerLeuGlyAsnLeuLysAsnLeuT 	uLysThrLeuSerIleHisAspLeuGlnAsnGl 	SerProLeuThrIleGluAspGluArgHisIle 	erLeuValLeuSerThrCysLysAsnIleTyrS                     GTTTGGTCCTCAGCACCTGTAAGAACATTTATT	rSerLeuargLeuGlnIleLysargCysAlaGl 	LeuAsnLysGlnAspIleThrTyrLeuGlyLy                  TTGAATAAGCAAGATATCAGATATCTGGGGAA	rpLysGlnGluPheArgThrLeuGluValThr 	UAlaProGluThrTyrIleProSerArgAlaV 	AlaSerTrpGluLysAlaAlaGluAspThrGl 	ysalaSerAlaLeuAspPheIleLysLeuAsp 	CAGGGAACATCCCCGATTACTTATTTGACTTCTT

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seq_documentation_block:
ID AAH99581 standard; ct
XX
AC AAH99581;
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XX 16-OCT-2001 (first 6
        seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH99581
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23-DEC-1999;
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25-APR-2000;
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                                                                                                                                                                                                                                                                             dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                983
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antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
antibacterial; endocrine; cardiant; central nervous system; virucide;
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                                                                                     22-DEC-2000;
                                                                                                                            26-JUL-2001
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                                                                                                                                                                                                                                             neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; ulcer; HIV infection; human immunodeficiency virus;
        99US-0471275.
2000US-0488725.
2000US-0552317.
                                                                                                                                                                                                                                             disorder; ss.
                                                                                     2000WO-US35017
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alignment_block:
US-09-697-089-2 x AAH99581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, hematopoietic disorders, and the state of the sease 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells they are expressed in, such as: antiinflammatory; antirheumatic antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antilicer; osteopathic; dermatological; antiallergic; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulco
osteoporosis, severe combined immunodeficiency, eczema, allergic
rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
                                                                                                            433 GlnArgPheLysProLysTyrLysPhePheHisLysSerPheGlnGluTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH99166 to AAH99904 encode the human proteins given in AAM25225 AAM25963. The proteins can have activities based on the tissues a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 511-512; 1217pp; English.
                                                                                                                                                                                                                                        152 CAAAGGTTCAAGCCAAAGTATAAATTCTTTCACAAGTCATTCCAGGAGTA
                                                                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                                                                                                                                                                                                                                                                                          416 alAsnGluAspValLeuLeuThrThrGlyLeuLeuCysLysTyrThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 AlaSerAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2950 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 uGlyValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerV 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                              2001-457603/49.
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                                                                                                                                                            GlyIleHisMetGluGluAlaProGluThrTyrIleProSerArgAlaVa
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                                            hrLysLeuIleMetAspAsnIleLysMetAsnGluGluAspAlaIleLys
                                                                                       nArgLeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuT
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                                                                          ACGGCTGCCGGGTGGTCTGACTGACAGCTTGGGTAACTTGAAGAACCTTA
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03-SEP-2001

colon

cancer (first

antigen

entry)

colorectal carcinoma; Human; colon cancer; colon

SS

cancer antigen; encoding cDNA SEQ

diagnosis; IJ

detection;

NO:1253

Homo sapiens

seq\_name:

/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH34171

\_documentation\_block: AAH34171 standard;

CDNA;

ВP

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                                                     uAlaArgLeuValGLyTrpGlnPheAspAspAspAspLeuSerValIleT
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CAGGTGCTTTTAAACTAGTAACTGCT
                                           AGCTAGGCTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTTATTA
                                                                                     TTAGTCAGAAAACTTAGCCAAGTGTTATCCAAGTTAACTTTTCTGCAAGA
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PR PR XX
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    Quality:
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US-09-697-089-2 x AAH34171/rev
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                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AAH34171
                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                        2577
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                                                                                                                                                                                                                                                                      2727 CACAATTTGGTCAAACTGAGCATTCTTGATTTATCAGAAAATTACCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                 861 uLysAspGlyAsnGluAlaLeuHisGluLeuIleAspArgMetAsnValL
                                                                                                                                                                                                                                                                                  845 HisAsnLeuValLysLeuSerIleLeuAspLeuSerGluAsnTyrLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colo cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3017;
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful
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SerLeuSerSerLeuLeuLysHisLeuGluGluValProGlnLeuValLy
                                                                                                                                                            euGluGlnLeuThrAlaLeuMetLeuProTrpGlyCysAspValGlnGly
                                                                                                                                                                                               AAAAGATGGAAATGAAGCTCTTCATGAACTGATCGACAGGATGAACGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pages 666 to 682 and page 7053 of the sequence listing were ing at time of publication, meaning no sequences are present ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carids encoding 4277 human colon cancer-associated polypeptides, for preventing, diagnosing and/or treating colorectal cancers -
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99US-0163280.
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ID AAX58000 standard:
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                                                     The invention relates to an excessive ovulation animal, which is a transgenic animal with a totipotent cell containing a DNA fragment containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The excessive ovulation animal is useful for improving the productivity animals. The method can improve the productivity of a useful animal
                                                                                                                                                                                                          This sequence encodes a gonadotropic hormone The invention relates to an excessive ovulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-320709/27
P-PSDB; AAY14079.
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SAKAI H.
   5984
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Sequence

Quality: 653.00 Length: Ratio: 1.074 Gaps: ercent Similarity: 54.874 Percent Identity:	άš	
lignment_block: JS-09-697-089-2 x AAX58000		
lign seg 1/1 to: AAX58000 from: 1 to: 5984		
69 PheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheG 	heGlnAspLeuAs       ::  CTCCAGACCTTCA	85 1367
85 nG1yGlnSerLeuPheHisGlnThrSerG	luGlyAspL   :::::   AAAGCAATC	98 1417
98 euAspAsp	ATGGCACAGGGT	100 1467
ln#	lnAspLeuLysAs	107
:::: :AAGAGGCAAAGAATCTGAATGAGC	AGCAGCTGAGAGC	1517
107 pLeuTyrHisThrProSerPheLeuAsnPhe		17
10 AGCIIAIACCAGCGCCAGIIICCGCCACAIGICIIIGCI	CTIGATAICICIT	7967
118TyrProLeuGlyGluAspIleAs; :::	eAspIleIlePhe ::::    GTCTATT	128 1611
129 AsnLeuLysSerThrPheThrGluProValLeuTrpArg	gLysAspGlnHi	4.5
2GCTTCAAAACACATCAGCAAACCTGTG.		6
143 SHISHISALGYGID LUCIDLEUTHILEUGHASHGIJCHTEUGGIL 	ACTTGA	1678
162 inSerProCysIleIleGluGlyGluSerGlyLysGlyLy:   ::	SSerThrLeu  :::::    GACGGTCCTC	178 1728
179 LeuGlnArgIleAlaMetLeuTrpGlySerGlyLyScysL     ::::::      :::      :::         1729 CTGAAGAAATAGCTTTTCTGTGGGCATCTGGATGCTGTC	SLySAlaLeuTh      ::   TCCCCTGTTAAA	195 1778
195 rLysPheLysPheValPhePheLeuArgLeuSer ::::   ::::    :::    1779 CAGGTTCCAGCTGGTTTTCTACCTCTCCCTTAGTTCCACC.	ArgAlaGlnG     ;:: ACCAGACCAGACG	210 1828
210 lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIlo	GA :	226 1878
227 IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuA: :::: :::::::::::::::::::::::::::::::	SLeuArgGlnArgVa 2     :::::::   STTAAAGAATCAGGT 1	243 1928
243 lleuPheLeuLeuAspGlyTyrAsnGluPheLys 	LLysProGlnAsnC 2	258 1974
258 ysProGluIleGluAlaLeuIleLysGluAsnHisArgPh		27 <b>4</b> 2019
275 VallleValThrThrThrThrGluCysLeuArgHisIleA: :::::::::::::::::::::::::::::::::::	O Le	291 2069

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561 2900	AsnSerPheValGluCysGlyIleHisLeu	2851	
œ	TTCACTGCAGATGCAGTTACTTAGGGGATTGTGGCAAATTTGTCCAC	0	
551	hrThrGluGlnGluIleLeuLysAlaIle	540	
539 2800	rLeuGlnSerValLysasn	533 2751	
533 2750	laLysArgProI	517 2743	
516 2742	rgAlaValMetLysHisLeuAlaAlaValTyrGinHisGly :::    ::::::::     :::::::::      ::::::	503 2696	
503 2695	rTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrA:   ::::::::   ::::   ::::   ::::   ::::	486 2652	
486 2651	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh	470 2602	
469 2601	rgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThrLys        :::          :::    ::: TGAGGCTGATTGAACTCCTGGATTCAGATAGGCAGGAACATCAAGATTTG	453 2552	
453 2551	SPTOLYSTYTLYSPhePheHiSLYSSerPheGlnGluTyTThrAlaGlyA:	436 2502	
436 2501	ValLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLy	420 2452	
419 2451	ysPheAspPheGluLeuGlnAspValSerSerValAsnGluAsp    :::   :::  :::::::::::::::::::::::	405 2402	
405 2401	.SerLeuAspHisCysGlyAspLe :::::::        :::   AACTGTGTCCTCCTGTGGTGAGCT	389 2352	
388 2351	LysAsnLysHisLysHisLy :::       AGGAACAAA	373 2320	
372 2319	erHisThrGlnThrThrLeuPheHisThrPhe	356 2270	
356 2269	UPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS	339 2220	
339 2219	LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLe	323 2170	
322 2169	eulleArgGluValLeulleLysGlu :::::   ::::::: TATTACGGAAGCTCTTTTCACATAAT	308 2120	
308 2119	YALALeuThrAlaGluValGlyAspMetThrGL    :::  AGAGACCATTCTAGAGATCAAAGCATTTCCCTT	2070	

802	7 uLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuS ::::::: ::::	787
3743		3694
œ	6AsnGluGluAspAlaIleLysLeuAlaGluGlyLe	776
3693	TTTCAGTCATTCCTGAAGAATTTCCAAACTTCCACCATATGGAGAAATTA	3644
775		775
775 3643	9 uGlyAsnLeuLySAsnLeuThrLySLeuIleMetAspAsnIleLySMet. ::::::::::::::::::::::::::::::::::::	759 3594
759 3593	5AspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLe	745 3550
744 3549	9 luArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis ::::::::::::::::::::::::::::::::::	3500
729 3499	3 .AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspG::::::           :::	5 1
712 3449	7 CysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLys	697 3400
696 3399	0 euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg	680 3350
680 3349	uValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL               ::::::::::::::::::::::::::::::::	663 3300
3299		3292
663 -	7 ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl	647
646 3291	1 hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer ::: :::	631 3245
631 3244	6	626 3195
625 3194	8 GlyGlyAlametAlaSerTrpGlu	618 3145
₩.	:::	9
617	roAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr	603
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3044	TYTLEUPHEASPTYTLEUPHEASPTYTLEUPHEASPTHISTORY TO THE TOTAL TOT	2995
1 I	9:00 Dr. 200	7
593 2994	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp     :::      :::::    ::::::       :::   AATTCCTTCAAGGGAGAACACTGACTTTGGGTGCGCTTAACTTACAG	577 2948
2947		2901

2	/SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX5627	seq_name:
	GATGCAGATATTGCATTGCTT 4413	4390
	rValil	1008
1007 4389	euSerLysLeuTnrPheLeuGInGluAlaArgLeuValGlyTrpGlnPhe- :: :::    ::::::::    ::: TGTTACGACTACCAAGGCTCATTAGACTGAACATGTTAAGTTGGCTCTTG	991 4340
4339		4290
991		974
4289	CTGGACAACATGCCAAACTTGCAGGAGTTGGACATCTCCAGGCATTTCAC	4240
4239		4190
960		945
945 4189	yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuA  :::    	928 4158
4157	TIPATGLEUTITASPITAT	4108
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		917
916 4107	euLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsn ::::::	900 4058
4057	TTGATCCTTCCTACTGGGGATGGAATTTATCGAGTGGCCAAACTGATCA	4009
900		883
883 4008	AlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAl::::	. 3967
3966	erIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGlu::      :::    ::       :::    AGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAGGAAACATCAGAA	851 3917
3916	CTGA	3871
851		834
3870	TGTAAGAAACTCACAGAAATTAAGTTTTCGGATTCATTTTTT	3829
834	erAl	819
3828	CGGATTTTGGGTCTCTCATGACTATGCTTGTTTCC	3794
818		802
3793	TCAAAATTCTCCAAACCTTCATGTTTTCCATCTGAAGTGTAACTTCTTTT	3744

seq\_documentation\_block:
ID AAX56272 standard; cDNA to mRNA; 5984 BP.

XX
AC AAX56272;
XX
DT 20-JUL-1999 (first entry)
XX
DE Human apoptosis inhibiting protein encoding of the control of

Human apoptosis inhibiting protein encoding cDNA #1.

Human; apoptosis inhibitory protein; apoptotic disease; diagnosis; spinal muscular atrophy; ds.

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alignment_block:
US-09-697-089-2 x AAX56272
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Percent Similarity:
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                                                                       1639
                                                                                                                                       1568 CCGATCTGGCCACGGACCACTTGCTGGGCTGTGATCTGTCTATT..... 1611
                                                                                                                                                                                                                                                                                                                                                         1468 GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1368 GAGCCGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATC 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1321 TTTCTCCAAAATATGAAGTCC...TCTGCGGAAGTGACTCCAGACCTTCA 1367
                                                                                                                                                                                                                                                                                     1518 AGCTTATACCAGCGCCAGTTTCCGCCACATGTCTTTGCTTGATATCTCTT 1567
                                                                                                                                                                                                                                                                                                                                                                                                                             1418 TTGAAGATTCAATAGCAGTTGGTCCTATAGTGCCAGAAATGGCACAGGGT 1467
118
                                                                                                                                                                                                                                                                                                                  101 .....LeuAlaGlnAspLeuLysAs 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence encodes a human apoptosis inhibitory protein. The apoptosis inhibitory protein is useful for the elucidation of the mechanism of various apoptosis diseases such as human spinal muscular atrophy and the diagnosis, the prevention and the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of such diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 11-13; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New apoptosis inhibitory protein - useful for determining mechanism of various apoptotic diseases e.g. human spinal muscular atrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-323531/27.
P-PSDB; AAY09539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5984 BP; 1777 A; 1267 C; 1267 G; 1673 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 nGlyGln......SerLeuPheHisGlnThrSerGluGlyAspL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 PheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspLeuAs 85
                                                                                          sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG 162
                                                                                                                                                               AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi 145
                                                                     .....CAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGCAACTTGA 1678
                                                                                                                                                                                                                                                .....TyrProLeuGlyGluAspIleAspIleIlePhe 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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1.074
54.874
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Gaps: 42
Percent Identity: 23.736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 5984
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AGCTTCACAGCGCATCGAACTCCAT	AATGACAGTTTTCT ysalaGlyValAla	3350 697
rSerAlaThrSerLeuArgLeuGlnIleLysA  ::::::	silep :::	680
PheSerLysLeuAsnLysGlnAspIleThrTyrL 	uValThrLeuArgAsp      AGTCGATGTGAATGAT	663 3300
hePheAsnTrpLysGlnGluPheArgThrLeuG      TGTCTAG	ArgAlaValSerLeuP	647 3292
<pre>stGluGluAlaProGluThrTyrlleProSe :::    ::           GAAACTTTCTCCAAAGCAGTACAAGATTCCC</pre>	hrGlyGlyIleHisMet ::: TTAGTACTGGCTATTGG	631 3245
LysAlaAlaGluAspT 	GGATAATGTAAAGAGC	626 3195
MetalaSerTrpGlu	GlyGlyAlam :::::   TCTGCCTTTGAACCTA	618 3145
AlaSerAlaLeuAspPheIleLysLeuAspPheTyr     ;;;   AATCACAGGTGCCAACTATAGATCAGGACTATGCT	roasnCysal :::    AAACATGTTTTGACAA	603 3095
PhePheGluHisLeuP    ::     PhaGaCaTCaCCCAGAGCACATTTTTCAGTTCTGG	CCCAATACGAGGAAAT	598 3045
CAGAAAGCTTGTCATTGTTGAGGAGCATCCACTT	TyrLeuPheAsp    :::       TACTTTTTCGACCACC	594 2995
/sSerLeuTyrIleAsnSerGlyAsnIleProAsp 	laPhePheGlnGlyLy    :::      :: AATTCCTTCAAGGGAG	577 2948
ThrSerLysSerAlaLeuSerGlnGluPheGluA 	TyrGlnGluSer        ::::: TGCTTATCAAAGCAAC	562 2901
ysGlyIleHisLeu ;;;        ;TTTCAGAACATTTACTGGTTCTTGCCCTGAAAAC	AsnSerPhevalGlucysGl:       CTTACTTTTCAATGGTTTC	552 2851
<pre>uIleLeuLysAlaIleAsnIle ::::   ::::: GTTACTTAGGGGATTGTGGCAAATTTGTCCACAA</pre>	ThrThrGluGlnGl ;;; rrTCACTGCAGATGCA	540 2801
JASD           GAAAATGATGACTACTTAAAGCACCAGCCAGAAA	rLeuGlnSerValLys     ::::::::: ATTGGAGAATATATCT	533 2751
SerIleAlaLysArgProLeuTrpArgGlnGluSe    -   AAAGAGTC	CysLeuLeuGlyLeuS	517 2743
ilMetLysHisLeuAlaAlaValTyrGlnHisGly :::::::       !TGTGTCTCATTTGCTCCATTTAGTGGATAAC	rgAlaVa ::    AAGCAGGGCCCAAAAT	503 2696
ArgTyrThrCysGlySerSerValGluAlaThrA 	rTyrSerSerLeuLeu :   ::::::    CTACAACAATTTTTTG	486 2652
NACAAATCAACTCACCCATGATGACTGTAAGGG	GGACTGTATCATTTGA	2602

961 PheGluAsnLeuLy	945 laGlyAsnA ::     : 4190 CAATCAATCACA	928 yAlaPhePheGl  :::    4158 AGGTTTC	917 TrpArgLeuThrA   4108 ACTTTGAATGATG	900 eulysHisleuG :::::::: 4058 TCCAGCAGTGTC	883 aLeuMetLeuProTrpGlyC    :::        109 .TTGATCCTTCCTACTGGGG	867 AlaLeuHisGluLeuIleAs :::: 3967 AAATTTGCCTACATTTTAGG	851 erileLeuAspL ::      :::  3917 AGATATTAAATC	834 aAsnAlaValLy :::       3871 .CAAGCCGTCCC	819 ProCysAsp     3829TGTAAGAAA	802 erAspileGlyG       :::   : 3794 CGGATTTTGGGT	787 uLysasnLeuLy ::::    3744 TCAAAATTCTCC	776	3644 TTTCAGTCATTC	775	759 uGlyAsnLeuLy :        3594 CCTGTGCCTGAA	745AspLeuG	729 luArgHisIleT ::::: ::: 3500 AGGAACTGCTTC	713 .AsnIleTyrSe :::::: :: :: :: :: :: :: :: :: :: :: :	3400 AGCAGAGGCTTT
sGlnLeuValPhePheAspF	ArgValSerSerAspGlyTrpLeuAlaPl 	:lyLysAsnProLeuLysAsnPheGlnGl ::::::::::::::::::::::::::::::::::	SPThr   :::  ACAGCGTGGTGGAAATTGCC	issLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsn :: :	ysAspValGlnGlyS ::: ATGGAATTTATCGAG	SGluLeuIleAspArgMetAsnValLeuGluGln ::::::	IleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnG       :::   ::::::::::::::::::::::::::	snAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLe ::	LeuGluGluIleGlnLeuValSer           ::::: ::: CTCACAGAAATTAAGTTTTCGGAT	luGlyMetAspTyrIleValLysS ::     :::   ::: CTCTCATGACTATGCTTGTTTCC.	SLYSMetCySLeuPheHiSLeu .::::: AAACCTTCATGTTTTCCATCTG	AsnGluGluAspAlaIle	GAAGAATTTCCAAACTTCC		nLeuLysAsnLeuThrLysLeuIleMetAsp       :::   :::  CTGAAAGAACTGTCTGTGGATCTGGAGGGC	lnAsnGlnArgLeuProGlyGl   :::    :::   ::: AAGACCAAATCTTTCCTAAT	luArgHisIleThrSerValThrAsnLeuLysThrLeuS ::::: ::::::::::::::::::::::::::::::	.AsnTleTyrSerLeuMetValGluAlaSerProLeuT :::::: CTCTGTCACCAAGTGCTCCATAAGCAAGTTGGAACTCA	AGCAGAGGCTTTATAGAAAGCATCCGCCCAGCTCTTG
heSerTh	heMetGlyVal   :::  CTTTCAAGCA	.nLeuAsnLeuA :   :::   : :CCTAAAGCTTT	eArgIleLeuGl :        AGCAATCAGTGG		» ·· ₽	LeuThrAl	A — Iu	GA	CysCysLeuSerAl ::: TCATTTTT	erLeuSerSerGlu	ThrHisLeuS ::: GTGTAACTTCTTTT	eLysLeuAlaGluGlyLe       ::::: CAAACTAGTAAAATTAAT	ATATGGAGA		<pre>spAsnIleLysMet.        :::::: scaatataaaatgttt</pre>	LeuThrAspSerLe    :::: CTGGATAAGTT	.euSerIleHis   ::::: !TTGAAGTCTCAGGG	hrIleGluAspG :: :::: GCGCAGCCGAAC	AGCTGTCTAAGGC
974	960 4239	945 4189	928 4157	916 4107	900 4057	883 4008	866 3966	851 3916	83 <b>4</b> 3870	818 3828	802 3793	787 3743	3693	775	775 3643	759 3593	744 3549	729 3499	

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seq_documentation_block:
ID AAA39808 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4290
by hybridomas, prepared by fusing antibody-producing cells of mammals immunized with an immunogen containing residues 256-586 or 841-1052 of a 1403 residue amino acid sequence, fully defined in the specification, or their partial sequence, with a myeloma cell line. The monoclonal antibodies are for the study of apoptosis disease onset mechanism, disease diagnosis and development of drugs to prevent and treat apoptosis-related diseases. The quantitation method with the monoclonal antibodies is simple and accurate by using a biological specimen. This sequence encodes the human apoptosis inhibitory protein NAIP which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Simple and accurate quantitation of human apoptosis inhibitory protein (NAIP) with monoclonal antibodies, for disease diagnosis and development of drugs to prevent and treat apoptosis related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAIP; apoptosis inhibiting protein; monoclonal antibody; diagnosis; apoptosis disease onset mechanism; drugs development; prevention; treatment; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 31-34; 36pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY88053.
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                                                                                                                                                                                                                                                                                                                             This invention describes novel anti-NAIP monoclonal antibodies, produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-350731/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NAIP cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NISC-) JAPAN
(SAKA/) SAKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGCAGATGATATTGCATTGCTT 4413
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292..4503
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Sequence 5984 BP; 1777 A;

1267 C; 1267 G;

1673 T; 0 other;

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alignment_block:
US-09-697-089-2 x AAA39808
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2020 CTATTGATTGCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATACCT 2069
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                             275 ValIleValThrThrThrGluCysLeuArgHisIleArgGlnPheGl
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                                                                                                                                     lLeuPheLeuLeuAspGlyTyrAsnGluPhe....LysProGlnAsnC
                                                                                                                                                                                                            GTTACTGAAATGTGCATGAGGAACATTATCCAGCAGTTAAAGAATCAGGT
                                                                                                                                                                                                                                                                                                     lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr
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                                                                  ....GTCATAGGAAAACTGATTCAAAAAAACCACTTATCCCGGACCTGC
                                                                                                                                                                                                                                             IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa
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                                                                                                    ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet
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8	00	2951
1	heValGluCysGlyIleHisLeu56	552
50	AGATGCAGTTACTTAGGGGATTGTGGCAAATTTGTCCACAA 28	2801
ш	hrThrGluGlnGluIleLeuLysAlaIleAsnIle 55	540
00	:: RAAAATGATGACTACTTAAAGCACCAGCCAGAAA 28	2751
9	LeuGlnSerValLysAsn53	533
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4 د ۸	CANGGCCCAAAAIIGIGICICAIIIIGCICCAIIIIAGIGGAIAAC 2/	517
	ValMetLysHisLeuAlaAlaValTyrGlnHisGly 51	0
95	CTACAACAATTTTTTGAACTATGTCTCCAGCCTCCCTTCAACAA 269	2652
ω	TyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrA 50	486
51	GTATCATTGAAACAAATCAACTCACCCATGATGACTGTAAGCGC 26	2602
ō,	yAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh 48	470
01	:::	2552
9	gLeuSerSerLeuLeuThrSerHisGluProGluGluValThrLys 46	453
51	- :::        ::::       i AGTCCTGCCTTCCAAGAATTTCTTGCGGGGA 25	0
ω	roLysTyrLysPhePheHisLysSerPheGlnGluTyrThrAlaGlyA 45	4
01		2452
6	euThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLy 43	420
51	GAGTTTAATGATGATGATCTCGCAGAAGCAGGGGTTGATGAAGAT 2	0 0
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01	TCTTCTTGTGGTGAGCTGGCCTTGAAAGGGTTTTTTTTCATGTT 24	on o
	erLeuAspHisCvsGlvAspLeuAlaLeuGluGlvValpheSerHisL 40	မ
51		2320
8	sasnLysHisLysHisLysGlyValalaalaSeraspPheIlearg 38	373
19	CTGTTTTCAAGTCCTATATGGAACGCCTTTCCTTA 23	2270
2	isThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 37	356
69	CTGTGCTCATTGGTTTCAGTATCCTTTTGACCCAT 22	2220
σ	eValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS 35	339
19	TGGAAAGAACCAAAGTTTGCAGAAGATACAGAAAACTCCTCT 22	2170
9	lnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLe 33	323
69	ACATAATATGACTCGTCTGCGAAAGTTTATG 21	2120
Ν	uIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu 32	308
19	: : : : : : : : : : : : : : :	2070
õ	.yAspMetThrGluAspSerAlaGlnAlaL 30	291

802	III.veBenI.onI.veI.veMotCveI.onDhoHieI.on ThrHieI.onS	787
3743	TTGATCCAAATTTCA	3694
3693 787	TTTCAGTCATTCCT	3644 776
775		775
775 3643	uGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMet. :               :::       :::	759 3594
759 3593	ACAATCCAGTCACAAGACCAAATCTTTCCTAATCTGGATAAGTT	745 3550
744 3549	luArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis	729 3500
729 3499	AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspG::::::::::::::::::::::::::::::::::::	713 3450
712 3449	CysalaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLys	697 3400
696 3399	euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg	680 3350
680 3349	UVAlThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL 	3300
663 3299	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl      TGTCTAGA	647 3292
646 3291	hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer::: ::	63 <u>1</u> 3245
631 3244		626 3195
625 3194	GlyGlyAlaMetAlaSerTrpGlu	618 3145
617 3144	roAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr:::	603 3095
603 3094	PhePheGluHisLeuP	598 3045
597 3044	TyrLeuPheAsp	594 2995
593 2994	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp    :::     ::::      AATTCCTTCAAGGGAGAACACTGACTTTGGGTGCGCTTAACTTACAG	577 2948
577 2947	TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluA       :::::    :::        TGCTTATCAAAGCACACTGTTGCTGCGTGTTCTCCATTTGTTTTGC	2901

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seq_documentation_block:
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Neuronal apoptosis inhibitor protein; NAIP; diagnosis; gene therapy; cancer; AIDS; amyotrophic lateral sclerosis; spinal muscular atrophy; ds.
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                                                                                                         Neuronal apoptosis inhibitor protein (NAIP) cDNA.
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AGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAGGAAACATCAGAA 3966
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                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                        cDNA; 6124 BP
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pLeuTyrHisThrProSerPheLeuAsnPhe....

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alignment_block:
US-09-697-089-2 x AAT71265
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    Quality:
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                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A cDNA clone (AAT71265) codes for novel human neuronal apoptosis inhibitor protein (NAIP) (AAW20032). It was isolated from a human foetal spinal cord cDNA library by probing with the genomic insert in cosmid 25086, containing a CATT locus, and completion of gaps in the sequence by further library screenings. The NAIP gene, on chromosome 513.1, is about 56 kb long and has 18 exons (see also AAT71266). NAIP is a negative regulator of apoptosis, partic. neuronal apoptosis and, when deficient or absent, contributes to neurodegenerative phenotypes such as spinal muscular atrophy (SMA) and amyotrophic lateral sclerosis. NAIP nucleic acids are useful for protein expression in host-vector systems, as probes/primers, and in gene therapy to inhibit apoptosis for treatment of AIDS, neurodegenerative disease, myelodysplastic syndromes or ischaemic injury, or (antisense) to increase apoptosis.
                                                                                                                              1368 GAGCCGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATC
                                                                                                                                                                                            1321 TTTCTCCAAAATATGAAGTCC...TCTGCGGAAGTGACTCCAGACCTTCA
1468 GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC 1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New neuronal inhibitor of apoptosis - useful for diagnosing treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
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                                                                                         euAspAsp.....
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                            .....LeuAlaGlnAspLeuLysAs 107
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1518	AGCTTATACCAGCGCCAGTTTCCGCCACATGTCTTTGCTTGATATCTCTT 1	1567
118 1568	TyrProLeuGlyGluAspIleAspIleIlePhe 1 :::	.28
129	heThrGluProValLeuTrpArgLysAspGlnH ::::::::	.45
1612	AAAACACATCAGCAAACCTGTG	.638
145 1639	LSH1SArgValGluGlnLeuThrLeuAsnGlyLeuLeu	.62
162 1679	nSerProCysIleIleGluGlyGluSerGlyLysGlyI 	.78
179 1729	LeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTh 1	.778
195 1779	rLysPheLysPheValPhePheLeuArgLeuSerArgAlaGlnG 2 ::::   ::::	828
210 1829	lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr 2	878
227 1879	IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa 2 ::: :::::::::::::::::::::::::::::::	.928
243 1929	lLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnC 2	258 1974
258 1975	ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet 2	274 2019
275 2020	VallleValThrThrThrThrGluCysLeuArgHisileArgGlnPheGl 2 ::::::::::::::::::::::::::::::::::::	2069
291 2070	yAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaL 3 AGAGACCATTCTAGAGATCAAAGCATTTCCCTTTTATAATACTGTCTGT	119
308 2120	euIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu 3 :-:::   ::::::::::::::::::::::::::::::	)22 ?169
323 2170	LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLe 3:::    ::::::::::::::::::::::::::::::	139
339 2220	uPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS 3	156
356 2270	erHisThrGloThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 3    ::::::::   :::::::::::::::::::::::	172 1319
373 2320		188
989	.SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisL 4 :::::::::	05

244	AAGAGCTATATGGATATGCAGCGCAGGGCATCACCAG	3195
31	aAlaGl	626
194	TTGAACCTATGAATGAATGGGAGCGAAATTTAGC	3145
25	lyGlyAlaMetAlaSerTrpGlu	618
144	:    ATGTTTTGACAAATCACAGGTGCCAACTATAGATCAGGACTATGC	3095
17	snCysAlaSerAlaLeuAspPheIleLysLeuAspPheT	603
0	:::     	4
03	PhePheGluHisLeuP	59
397 3044	TyrleuPheAsp	594 2995
9	ACTGACTTTGGGTGCGCTTAACTTACAG	4
93	heGlnGlvLvsSerLeuTvrIleAsnSerGlvAsnIleProAs	577
7	TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluA	ഗ
900	CAGAACATTTACTGGTTCTTGCCCT	2851
61	lGluCysGlyIleHisLeu :::	552
2850	TICACTGCAGATGCAGTTACTTAGGGGATTGTGGCAAATTTGTCCAC	2801
51	rThrGluGlnGluIleLeuLysAlaIl	540
39	TLEUGInSerVallysAsn	533 2751
750		2743
33	lus	517
516 2742	rgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGly 5 ::    ::::::::::::::        AAGCAGGGCCCAAAATTGTGTCTCATTTGCTCCATTTAGTGGATAAC 2	503 2696
2695	TTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrA 5:   :::::::   ::::   ::::   ::::   ::::   ::::	486 2652
186 2651	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh 4     :::   :::::::	470 2602
169	rgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThrLys 4        ::           ::    :: TGAGGCTGATTGAACTCCTGGATTCAGATAGGCAGGAACATCAAGATTTG 2	453 2552
153 2551	SPTOLYSTYTLYSPhePheHisLysSerPheGlnGluTyrThrAlaGlyA 4 :       :::   ::: ACCATTCTACCGGTTTTTAAGTCCTGCCTTCCAAGAATTTCTTGCGGGGA 2	436 2502
136	ValLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLy 4	420 2452
119 2451	ysPheAspPheGluLeuGlnAspValSerSerValAsnGluAsp 4    :::   :::  ::::::   :::	405 2402

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900 euLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsn 916
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                                                                                                                        aLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuL 900
                                                                                                                                                                                                                                             AlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAl
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                                                          . TTGATCCTTCCTACTGGGGATGGAATTTATCGAGTGGCCAAACTGATCA
                                                                                                                                                                                  AAATTTGCCTACATTTTAGGTTCTCTTAGTAACCTGGAAGAA.....
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seq_documentation_block:
ID AAT71264 standard; cDNA; 6133 BP
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                                                                                                                                                                                                                                                                                                                                                                         Key
exon
A new neuronal apoptosis inhibitor protein (NAIP) cDNA clone
                               Example 4; Fig 5A-L; 102pp; English.
                                                            New neuronal inhibitor of apoptosis - useful for diagnosing and treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuronal apoptosis inhibitor protein; NAIP; diagnosis; gene therapy; cancer; AIDS; amyotrophic lateral sclerosis; spinal muscular atrophy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT71264;
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                                                                                                                WPI; 1997-385335/35.
                                                                                                                                              Korneluk RG, Mackenzie AE,
                                                                                                                                                                                                             19-JAN-1996;
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                                                                                                                                                                                                                                                                           24-JUL-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuronal apoptosis inhibitor protein (NAIP) cDNA (with exon
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                                                                                                                                                                             (UYOT-) UNIV OTTAWA.
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                                                                                                                                              Robertson G,
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alignment_block:
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Percent Similarity:
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1788 CAGGTTCCAGCTGGTTTCTACCTCTCCCTTAGTTCCACCAGACCAGACG 1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
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                                                           195 rLysPheLysPheValPhePheLeuArgLeuSer....ArgAlaGlnG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 pLeuTyrHisThrProSerPheLeuAsnPhe.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     injury, or (antisense) to increase apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 nGlyGln.....SerLeuPheHisGlnThrSerGluGlyAspL
                                                                                                                                                                                     LeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTh 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC 1526
                                                                                                                                 CTGAAGAAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCCTGTTAAA 178;
                                                                                                                                                                                                                                                                                                                                                                                                           .....CAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGCAACTTGA 1687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....LeuAlaGlnAspLeuLysAs 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGAAGATTCAATAGCAGTTGGTCCTATAGTGCCAGAAATGGCACAGGGT 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....TyrProLeuGlyGluAspIleAspIleIlePhe 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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54.874
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Gaps: 42
Percent Identity: 23.736
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503 2704	TTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrA:   ::::::   :::   :::   :::   :::   :::   :::   :::   :::   ::::	486 2661
486 2660	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh 	470 2611
469 2610	rgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThrLys        :::           :::    ::: TGAGGCTGATTGAACTCCTGGATTCAGATAGGCAGGAACATCAAGATTG	453 2561
453 2560	SPIOLYSTYTLYSPhePheHiSLYSSErPheGlnGluTyTThrAlaGlyA:	436 2511
436 2510	ValleuleuThrThrGlyLeuleuCysLysTyrThrAlaGlnArgPheLy	420 2461
419 2460	ysPheAspPheGluLeuGlnAspValSerSerValAsnGluAsp    :::   :::   :::   SerSerValAsnGluAsp   SerSerValAsnGluAsp	405 2411
405 2410	SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSerHisL::::::::	389 2361
388 2360	LysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIleArg::        	373 2329
372 2328	erHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 	356 2279
356 2278	uPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS        :::	339 2229
339 2228	LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLe :::    :::::	323 2179
322 2178	euIleArgGluValLeuIleLySGluLeuAlaGluGlyLeuLeu :::::   ::::: ### PATTACGGAAGCTCTTTCACATAATATGACTCGTCTGCGAAAGTTTATG	308 2129
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291 2078	ValileValThrThrThrThrGluCysLeuArgHisileArgGlnPheGl::::::::::::::::::::::::::::::::::::	275 2029
274 2028	ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet	258 1984
258 1983	lLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnC                 CTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA	243 1938
243 1937	IleargLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa ::: GTTACTGAAATGTGCATGAGGAACATTATCCAGCAGTTAAAGAATCAGGT	227 1888
226 1887	lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr        ::: :::            ::: AGGGGCTGGCCAGTATCATCTGTGACCAGCTCCTAGAGAAAGAA	210 1838

744	luArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis	729
729 3508	AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspG 	713 3459
712 3458	CysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLys	697 3409
696 3408	euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg	680 3359
680 3358	<pre>3 uValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL         :::::    :::::::::::::::::::::</pre>	663 3309
663 3308	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl      TGTCTAGA	647 3301
646 3300	hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer 	631 3254
631 3253	S	626 3204
625 3203	GlyGlyAlametAlaSerTrpGlu	618 3154
617 3153	roAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr :::	603 3104
603 3103	CCCAATACGAGGAAATAAGACATCACCCAGAGCACATTTTTCAGTTCTGG	598 3054
597 3053	TyrLeuPheAsp	594 3004
593 3003	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp    :::     :::::    :::::::    :::   AATTCCTTCAAGGGAGAACACTGACTTTGGGTGCGCTTAACTTACAG	577 2957
577 2956	TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluA       ::::      TGCTTATCAAAGCAACACTGTTGCTGCGTGTTCTCCATTTGTTTTGC	562 2910
561 2909	Reference   AsnSerPheValGluCysGlyIleHisLeu	552 2860
551 2859	ThrThrGluGlnGlu ::: :::::::::::::::::::::::::::::::::	540 2810
539 2809	rLeuGlnSerVa     ::::::: ATTGGAGAATAT	533 2760
533 2759	7 CysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGlnGluSe :::      2AAAGAGTC	517 2752
2751	::      aagcagggcccaaaartgtgtctcatttgctccatttagtggataac	2705

1007 4398	1 euSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPhe ::::::    ::: 9 TGTTACGACTACCAAGGCTCATTAGACTGAACATGTTAAGTTGGCTCTTG	99 434
991 4348	4 rLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGlnValL  ::: :::           :: :::           :: ::	97 429
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960 4248	5 laGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMetGlyVal ::         ::::::::::::::::::::     ::: 9 CAATCAATCACAAGATTACAGAGGAAGGATACAGAAATTTCTTTC	94 419
945 4198	8 yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuA  :::      :::    :::    :::    7 AGGTTTCCAGAAACTTGAGAACCTAAAGCTTT	928 4167
928 4166	TrpArgLeuThrAspThr	917 4117
916 4116	0 euLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsn :::::::         :::::: 7 TCCAGCAGTGTCAGCAGCTTCATTGTCTCCGAGTCCTCCTCATTTTTCAAG	900 4067
900 4066	aLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuL    :::       	883 4018
883 4017	7 AlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAl ::::       ::: 6 AAATTTGCCTACATTTTAGGTTCTCTTAGTAACCTGGAAGAA	86 397
866 39 <b>7</b> 5	1 erIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGlu::       :::     :::::::::::::::::::::	392
851 3925	4 aAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuS :::       :::::    :::	83 388
834 3879	9 ProCysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAl	81 383
818 3837	2 eraspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGlu      :::   :::     3 CGGATTTTGGGTCTCTCATGACTATGCTTGTTTCC	380
802 3802	7 uLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuS ::::    ::::    :::::   3 TCAAAATTCTCCAAACCTTCATGTTTTCCATCTGAAGTGTAACTTCTTTT	78 375
787 3752	6	77 370
3702	3 TTTCAGTCATTCCTGAAGAATTTCCAAACTTCCACCATATGGAGAAATTA	365
775	G	77
775 3652	9 uGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMet. ::::       :::   :::         ::::  3 CCTGTGCCTGAAAGAACTGTCTGTGGATCTGGAGGGCAATATAAATGTTT	360
759 3602	AspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLe :::    :::   :::    aCAATCCAGTCACAAGACCAAATCTTTCCTAATCTGGATAAGTT	74 355
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DT 06-OCT-1997 (first entry)
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                                                                                                                                                                                           exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuronal apoptosis inhibitor protein (NAIP) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspAspAspAspLeuSerValIle 1015
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alignment_block:
US-09-697-089-2 x AAT71266
                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibitor protein (NAIP) (AAM702033). It was isolated from a human foetal spinal cord cDNA library by probing with the genomic insert in cosmid 25086, containing a CATT locus, and completion of gaps in the sequence by further library screenings. The NAIP gene, on the sequence by further library screenings. The NAIP gene, on chromosome 5q13.1, is about 56 kb long. NAIP is a negative regulator of apoptosis, partic neuronal apoptosis and, when deficient or absent, contributes to neurodegenerative phenotypes such as spinal muscular atrophy (SMA) and amyotrophic lateral cuseful for protein expression in host-vector systems, as probes or primers, and in gene therapy to inhibit apoptosis for treatment of AIDS, neurodegenerative disease, myelodysplastic syndromes or ischaemic injury, or (antisense) to increase apoptosis.
                                                                                                                                                                                                                                                 Align seg 1/1 to: AAT71266
                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                    1425 TTTCTCCAAAATATGAAGTCC...TCTGCGGAAGTGACTCCAGACCTTCA
1572 GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC
                                                                                                                        1472 GAGCCGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATC
                                                             1522 TTGAAGATTCAATAGCAGTTGGTCCTATAGTGCCAGAAATGGCACAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6228 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New neuronal inhibitor of apoptosis - useful for diagnosing treating, e.g. cancer, AIDS or amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW20033
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                                                                                                                                                    85 nGlyGln.....SerLeuPheHisGlnThrSerGluGlyAspL
                                                                                                                                                                                                                  69 PheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspLeuAs
                            .....LeuAlaGlnAspLeuLysAs 107
                                                                                   euAspAsp.....
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                                                                                                                                                                                                                                                 from: 1
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Gaps:
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41
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405	vsGlvAsp	389
388 2455	LysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIleArg::       	373 424
372 2423	erHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 	356 374
356 2373	UPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS       :: 	339
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322 2273	euIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu :::::   :::::::::::::::::::::::::::::	308 224
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226 1982	lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr	210 933
210 1932	TLYSPheLySPheValPhePheLeuArgLeuSerArgAlaGlnG::::   :::::	195 883
195 1882	leAlaMetLeuTrpGlySerGly      :::        TAGCTTTTCTGTGGGCATCTGGA	179 833
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128 1715	TyrProLeuGlyGluAspIleAspIleIlePhe :::	118 672
1671	g :	622

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uLysAsnLeuLysLysMetCysLeuPheHisLeu.....ThrHisLeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTGTCACCAAGTGCTCCATAAGCAAGTTGGAACTCAGCGCAGCCGAAC
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                                                                                                                                                                                                                        aAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGATTTTGGGTCTCATGACTATGCTTGTTTCC........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAAATTCTCCAAACCTTCATGTTTTCCATCTGAAGTGTAACTTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGATCCAAATTTCAGCTGAGTATGATCCTTCCAAACTAGTAAAATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCAGTCATTCCTGAAGAATTTCCAAACTTCCACCATATGGAGAAATTA 3797
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                                                 aLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuL
                                                                                              AAATTTGCCTACATTTTAGGTTCTCTTAGTAACCTGGAAGAA.....
                                                                                                                                             AlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                    ProCys...AspLeuGluGluIleGlnLeuValSerCysCysLeuSerAl
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                                                                                                                                                                                             AGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAGGAAACATCAGAA
                                                                                                                                                                                                                                                                                                                                                                                       ...TGTAAGAAACTCACAGAAATTAAGTTTTCGGATTCATTTTTT.....
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.CAAGCCGTCCCATTTGTTGCC...AGTTTGCCAAATTTTATTTCTCTGA 4020
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ID AAX58001 standard; cD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4509 GCATTGCTT 4517
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    This sequence encodes a gonadotropic hormone. The invention relates to an excessive ovulation animal, which is a transgenic animal with a totipotent cell containing a DNA fragment containing a promoter sequence and a gonadotropic hormone coding sequence. The DNA fragment is in the somatic cell chromosome. The
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-320709/27.
P-PSDB; AAY14080.
                                                                                                                                                                                                                                                                                                                   An excessive ovulation animal - useful for improving productivity of animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gonadotropic hormone; excessive ovulation animal; transgenic animal; totipotent cell; somatic cell chromosome; ds.
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                                                                                                                                                                                                                                          Claim 1; Page 9-11; 18pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KAGA-) KAGAKU GIJUTSU
(SAKA/) SAKAI H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTCATTAGACTGAACATGTTAAGTTGGCTCTTGGATGCAGATGATATT 4508
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Quality:
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Ratio: 1.023
Percent Similarity: 53.016
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                                                                                                                                     1879
                                         1829
                                                                                                                                                                                                                                                                                                         162 lnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeu 178
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1679 aCTCTGTCATGTGTGGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTC 1728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1518 AGCTTATACCAGCGCCAGTTTCCGCCACATGTCTTTGCTTGATATCTCTT 1567
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                                                                                  243 lLeuPheLeuLeuAspGlyTyrAsnGluPhe....LysProGlnAsnC 258
                                                                                                                                                                                                                                               210 lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 .....LeuAlaGlnAspLeuLysAs 107
                                                                                                                                                                            227 IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa 243
258 ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    excessive ovulation animal is useful for improving the productivity of animals. The method can improve the productivity of a useful animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 nGlyGln......SerLeuPheHisGlnThrSerGluGlyAspL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 PheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspLeuAs 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TyrProLeuGlyGluAspIleAspIleIlePhe 128
                                                                                                                                GTTACTGAAATGTGCATGAGGAACATTATCCAGCAGTTAAAGAATCAGGT 1928
                                                                                                                                                                                                                      .....CAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGCAACTTGA 1678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 1094
Gaps: 42
Percent Identity: 23.675
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551	ThrThrGluGlnGluIleLeuLysAlaIleAsnIle	540	
2800	TTGGAGAATATATCTGAAAATGAT	2751	
539	GlnSerValLysAsn	533	
7		2743	
533	gGlnGluS	517	
516 2742	rgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGly ::    ::::::::::       aagCagGgCCCaAaAaTTGTGTCTCATTTGCTCCATTTAGTGGATAAC	2696	
6	CAACAATTTTTTGAACTATGTCTCCAGCCTCCCTTCAACA	, Gi	
503	yrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaTh	486	
486 2651	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh      :::   :::::       GACTGTATCATTTGAAACAAATCAACTCACCCATGATGACTGTAAGCGC	470 2602	
2601		2552	
469	LeuSerSerLeuLeuThrSerHisGluProGluG	453	
453 2551	SPIOLYSTYPLYSPHEPHOHISLYSSEPPHOGINGLUTYTTHTALAGLYA :       :::   ::: :::       :::        :::         :::         :::	4 3 6 2502	
ı ö	AAGATCTAACCATGTGCTTGATGAGCAAATTTACAGCCCAGAGACTAA	, in	
436	alLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPhe	42	
4	:::   ::: 	2402	
419	eAspPheGluLeuGlnAspValSerSerValAsnGluA	405	
405 2401	SerLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSezHisL :::::::                 ::	2352	
· ·	GAACAAAGCGACAGCTGAAATTCTCAAAG	N.	
Ó	HisLysHisLysGlyValAlaAlaSerAspPheIleArg.	37	
	TTTGATGATGTGGCTGTTTTCAAGTCCTATATGGAAGGCCTTTCCT	2270	
372	<b>ThrGlnThrThrLeuP</b>	356	
356 2269	uPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS        :::	2220	
2219	TACTTTGGAAAGAACCAAAGTTTGCAGAAAGATACAGAAAACTCCT	7	
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322 2169	euIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu :::::   :::::::::::::::::::::::::::::	308 2120	
2119	AGAGACCATTCTAGAGATCAAAGCATTTCCCCTTTTATAATACTGTCTGT	2070	
308	luValGlyAspMetThrGluAspSerAlaGlnAla	291	
291 2069	ValileValThrThrThrThrGluCysLeuArgHisIleArgGlnPheGl::::::::::::::::::::::::::::::::::::	275 2020	
2019	GTCATAGGAAAACTGATTCAAAAAAAACCACTTATCCCGGACCTGC	1975	

202	Ţ₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽₽	3644
775		775
775 3643	UGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMet.::::::::::::::::::::::::::::::::::::	759 3594
759 3593	AspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLe :::    :::   :::    :::    :::     ::::     ::::      ::::       aCAATCCAGTCACAAGACCAAATCTTTCCTAATCTGGATAAGTT	745 3550
744 3549	luargHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis ::::::::::::::::::::::::::::::::::	729 3500
729 3499	.AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspG ::::::    :::: CTCTGTCACCAAGTGCTCCATAAGCAAGTTGGAACTCAGCGCAGCCGAAC	713 3450
712 3449	CysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLys	697 3400
696 3399	euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg 	680 3350
680 3349	UValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL       :::::   ::::::::::::::::::::::::	663 3300
663 3299	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl	647 3292
646 3291	hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer:::::::::::::::::::::::::::::::::::	631 3245
631 3244		626 3195
625 3194	GlyGlyAlaMetAlaSerTrpGlu	618 3145
617 3144	roAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr :::         ::           :: AAACATGTTTTGACAAATCACAGGTGCCAACTATAGATCAGGACTATGCT	603 3095
603 3094	PhePheGluHisLeuP	598 3045
597 3044	TyrLeuPheAsp	594 2995
593 2994	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp     ::      ::::	577 2948
577 2947	TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluA	562 2901
561 2900	AsnSerPheValGluCysGlyIleHisLeu	552 2851
	TTCACTGCAGATGCAGTTACTTAGGG	0

	ũ	: /SIDS2/qcqdata/qeneseq/qeneseqn/NA1999.DAT:AAX5627	seq_name:	seq
		TCAAATCTGCGTTCTTGCCACCTGGTGTTTTA 4386	4355	
		LysGluPheLeuProAspProAlaLeu 983	975	
_	974 4354	tGlyValPheGluAsnLeuLySGlnLeuValPhePheAspPheSerThr. :::	958 4305	
-	958 4304	LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMe     :::   :::::      	942 4255	
-	941 4254	hePheGlyLysAsnProLeuLysAsnPheGlnGln:::::                ::::	930 4205	
_	930 4204	GCTTGCATGGAAGCCAGTGGTATAGCCAAGCTTTCTGCTGCAACATGTCT	929 <b>4</b> 155	
-	928 4154	TrpArgLeuThrAspThrGluIleArgIleLeuGly	917 4108	
•	916 4107	euLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsn:::::::::::::::::::::::::::::::::::	900 4058	
•	900 4057	aLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuL	883 4009	
w	883 4008	AlaLeuHisGluLeuTleAspArgMetAsnValLeuGluGlnLeuThrAl:::	867 3967	
O.	866 3966	erIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGlu::      :::   ::::::::::::::::::::::::	851 3917	
O1	851 3916	aAsnalaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuS :::       :::::	834 3871	
Ü	83 <b>4</b> 3870	ProCysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAl	819 3829	
w	818 3828	erAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGlu      :::   ::: 	802 3794	
w	802 3793	uLysasnLeuLysLysMetCysLeuPheHisLeuThrHisLeuS ::::    :::    TCAAAATTCTCCAAACCTTCATGTTTTCCATCTGAAGTGTAACTTCTTTT	787 3744	
w	787 3743	TTGATCCAAATTTCAGCTGAGTATGATCCTTCCAAACTAGTAAAATTAAT	776 3694	

seq\_documentation\_block:
ID AAX56273 standard; cDNA to mRNA; 5366 BP.

XX
AC AAX56273;
XX
DT 20-JUL-1999 (first entry)
XX
DE Human apoptosis inhibiting protein encoding of XX
KW Human; apoptosis inhibitory protein; apoptot.

Human; apoptosis inhibitory protein; apoptotic disease; diagnosis;

Human apoptosis inhibiting protein encoding cDNA #2.

spinal muscular

atrophy; ds

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alignment_scores:
Quality:
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US-09-697-089-2 x AAX56273
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Percent Similarity:
  1639
                                                                                          1612
                                                                                                                                                                                                                                                                                  1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1368 GAGCCGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATC 1417
                                                                                                                                                                                1568 CCGATCTGGCCACGGACCACTTGCTGGGCTGTGATCTGTCTATT..... 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1321 TTTCTCCAAAATATGAAGTCC...TCTGCGGAAGTGACTCCAGACCTTCA 1367
                                                                                                                                                                                                                                   118
                                                                                                                                         129
                                                                                                                                                                                                                                                                                                                                                                            1468 GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC 1517
                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human apoptosis inhibitory protein. The apoptosis inhibitory protein is useful for the elucidation of the mechanism of various apoptosis diseases such as human spinal muscular atrophy and the diagnosis, the prevention and the treatme of such diseases.
                                                                                                                                                                                                                                                                                                                       New apoptosis inhibitory protein - useful for determining mechanism of various apoptotic diseases e.g. human spinal muscular atrophy
                                            145 sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5366 BP; 1483 A; 1173 C; 1222 G; 1488 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 13-15; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-323531/27.
P-PSDB; AAY09540.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 euAspAsp..... 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .85 nGlyGln.....SerLeuPheHisGlnThrSerGluGlyAspL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 PheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspLeuAs
                                                                                                                   AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi 145
                                                                                                                                                                                                                                                                               AGCTTATACCAGCGCCAGTTTCCGCCACATGTCTTTGCTTGATATCTCTT 1567
                                                                                                                                                                                                                                                                                                                                                                                                                 .....LeuAlaGlnAspLeuLysAs 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGAAGATTCAATAGCAGTTGGTCCTATAGTGCCAGAAATGGCACAGGGT 1467
.....CAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGCAACTTGA 1678
                                                                                                                                                                                                             .....TyrProLeuGlyGluAspIleAspIleIlePhe 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97JP-0280831.
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1.023
53.016
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Gaps: 42
Percent Identity: 23.675
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                                                                                          1638
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s x

469	rgArgLeuSerSerLeuLeuThrSerHisGluProGluGluValThrLys	453
is i		õ
453	ProLysTyrLysPhePheHisLysSerPheGlnGluTyrThrAlaGl	436
436 2501	ValleuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLy	420 2452
419 2451	ysPheAspPheGluLeuGlnAspValSerSerValAsnGluAsp    :::   ::: :::   ::: :::::   ::        CTTTGAGTTTAATGATGATGATCTCGCAGAAGCAGGGGTTGATGAAGAT	
405 2401	Cyscly         TGTGGT	389 2352
388 2351	ysHisLysGlyValAlaAl    :: GCGAC	373 2320
372 2319	erHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 	356 2270
356 2269	uPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS        ::: 	339 2220
339 2219	LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLe :::    :::::	323 2170
322 2169	euIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu ::::   :::::: TATTACGGAAGCTCTTTTCACATAATATGACTCGTCTGCGAAAGTTTATG	308 2120
308 2119	yAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaL     ::: 	291 2070
291 2069	ValIleValThrThrThrThrGluCysLeuArgHisIleArgGlnPheGl	275 2020
274 2019	ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet	258 1975
258 1974	lLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnC               	.1929
243 1928	IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa ::: ::::::::::::::::::::::::::::::::	227 1879
226 1878	lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr 	210 1829
210 1828	xLysPheLysPheValPhePheLeuArgLeuSerArgAlaGlnG::::   ::::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::: :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::: :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::: :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::: :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::: ::: :::  :::  :::  :::  :::  ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::::	195 1779
195 1778	LeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTh	179 1729
178 1728	: InSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeu ::    ::    ::          ::     ::	162 1679

696	<pre>euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg  </pre>	680
3349	TGTAGGCCAGGA	3300
680	alThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyr	663
663 3299	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl	647 3292
Ñ	ACTGGCTATTGGAAACTTTCTCCAAAGCAGTACAAGATTC	
646	yGlyIleHisMetGluGluAlaProGluThrTyrIleProS	631
3244	GGATAATGTAAAGAGCTATATGGATATGCAGCGCAGGGCATCACCAGACC	3195
631	sAlaAlaGl	626
	:::	4
625	lyGlyAlaMetAlaSerTrpGlu	618
3144		3095
617	snCysAlaSerAlaLeuAspPheIleLysLeuAspPh	603
3094	ACATCACCCAGAGC	3045
603	heGluHisLe	598
3044	ACTITITE	2995
597	euPheAs	594
2994	AATTCCTTCAAGGGAGAACACTGACTTTGGGTGCGCTTAACTTACAG	2948
593	hePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProA	577
2947	ATCAAAGCAACACTGTTGCTGCGTGTTCTC	2901
577	GlnGluSerThrSerLysSerAlaLeuSe	562
2900	TACTGGT	2851
561	heValGluCysGlyIleHisL	552
2850	TTTCACTGCAGATGCAGTTACTTAGGGGATTGTGGCAAATTTGTCCACAA	2801
551	hrThrGluGlnGluIleLeuLysAlaIl	540
2800	GATGACTACTTAAAG	2751
539	GlnSerValLysAsn	533
2750	:::     AAAGAGTC	2743
533	. L	517
516 2742	rgAlaValMetLysHisLeuAlaAlaValTyrGlnHisGly ::    ::::::      AAGCAGGGCCCAAAATTGTGTCTCATTTGCTCCATTTAGTGGATAAC	503 2696
2695	ACAACAATTTTTTGAACTATGTCTCCAGCCTCCCTTCAAC	2652
503	TyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaTh	486
486 2651	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh     :::   ::::::     GGACTGTATCATTTGAAACAAATCAACTCACCCATGATGACTGTAAGCGC	470 2602
2601		2552

941 4254	hePheGlyLysAsnProLeuLysAsnPheGlnGln ::: ATGTBABAGATTTGCCCCTCTBGBAGATTTTCBAGCCCCTTCCTCATTTTCA	930 4205
4204	GCTTGCATGGAAGCCAGTGGTATAGCCAAGCTTTCTGCTGCAAC	4155
930		929
928 4154	TrpArgLeuThrAspThrGluIleArgIleLeuGly	917 4108
916 4107	euLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsn ::::::::	900 4058
900 4057	aLeuMetLeuProTrpG1yCysAspValGlnG1ySerLeuSerSerLeuL    :::      	883 4009
883 4008	AlaLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAl::::::::::::::::::::::::::::::::::::	867 3967
866 3966	erIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGlu ::      ::   AGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAGGAAACATCAGAA	851 3917
851 3916	AASNAlaValLySIleLeuAlaGlnAsnLeuHisAsnLeuValLySLeuS:::       :::::	834 3871
83 <b>4</b> 3870	ProcysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerAl	819 3829
818 3828	eraspileGlyGluGlyMetaspTyrileValLysSerLeuSerSerGlu	802 3794
802 3793	ULYSASnLeuLySLySMetCySLeuPheHisLeuThrHisLeuS	787 3744
787 3743	_	776 3694
3693	TTT	3644
775		775
775 3643	uGlyAsnLeuLysAsnLeuThrLysLeuIleMetA :        :::   ::: CCTGTGCCTGAAAGAACTGTCTGTGGATCTGGAGG	759 3594
759 3593	ACAATCCAGTCACAAGACCAAATCTTTCCTAATCTGGATAAGTT	745 3550
744 3549	luargHisIleThrSerValThrAsnLeuLysThr :::: AGGAACTGCTTCTCACCCTGCCTTCCCTGGAATCT	729 3500
729 3499	.AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspG    ::::::           :::   :::	713 3450
712 3449	CysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLys	697 3400
3399	TAATGACAGTTTTCTCAGCTTCACAGCGCATCGAACTCCATT	3350

CTATCATACTGTTCCTTCTAGTGTCCTTCTGTGGATTTAGGCGCATTCTG 4304

LeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuAlaPheMe 958

942

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seq_documentation_block:
ID AAT30092 standard;
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                This sequence represents the cDNA sequence for the human neuronal apoptosis inhibitor protein (NAIP). This sequence was found on a region of the human chromosome 5q13. This sequence was isolated from a yeast artificial chromosome 5q13. This sequence was isolated from a yeast artificial chromosome (YAC) contig containing the D58435-D58112 interval of the chromosome 5q13. Mutations in this gene, are causative of spinal muscular atrophy (SMA) types I, II, and III. SMAs are a group of autosomal recessive, neurodegenerative disorders. SMAs are classified into the three types based upon the age of onset (with type I being the severest form with the earliest age of onset). All three types are characterised by the degeneration of the alpha motor neurons of the spinal cord manifesting as weakness and wasting of the proximal voluntary muscles. The most common mutations of this sequence are thought to be deletions of exons 5 and 6, and reductions in the copy number of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuronal apoptosis inhibiting protein; human; NAIP; chromosome 5q13; YAC; yeast artificial chromosome; spinal muscular atrophy; mammallan cell; autosomal recessive; neurodegenerative disorder; alpha motor neuron; SMA; spinal cord; proximal voluntary muscle; therapy; apoptotic mechanism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 64-67; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuronal apoptosis inhibitor for use in the diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-222003/22.
P-PSDB; AAR89217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1994;
18-OCT-1994;
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(UYOT-) UNIV OTTAWA.
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This gene, (and primers and probes based on this gene)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Korneluk RG,
Roy N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEV CORP
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94GB-0021019
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alignment_block:
US-09-697-089-2 x AAT30092
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for the diagnosis of SMA, and for directing the formulation of conventional and genetic therapies for SMA. Identification of genes showing homology with the NAIP locus, and proteins that interact with NAIP can be used in the elucidation of apoptotic mechanisms in mammalian
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                                                                                                                                                                                                                                                                                                                                LeuGlnArgIleAlaMetLeuTrpGlySerGlyLySCysLysAlaLeuTh
                                                               GTTACTGAAATGTGCATGAGGAACATTATCCAGCAGTTAAAGAATCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                         lnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeu
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                                                                                                    IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa
                                                                                                                                                                                       lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr
                                                                                                                                                                                                                                                                   rLysPheLysPheValPhePheLeuArgLeuSer.....ArgAlaGlnG
                                                                                                                                                                                                                                                                                                               CTGAAGAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCTGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG
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                                                                                                                                             ACTCTGTCATGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTC
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Gaps: 33
Percent Identity: 24.120
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                   .LysProGlnAsnC
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2904	TGGAGAATATATCTGAAAATGATGACTACTTAAAGCACCAGCCAG	2855
539	rLeuGlnSerValLysAsn	
2854	AAAGAGTC	2847
533	lnGluSe	517
<b>ω</b> 1	GGCCCAAAATTGTGTCTCCATTTGCTCCATTTAGTGGATAAC	0
16	AlaValMetLvsHisLeuAlaAlaValTvrGlnHisGlv	50
503 2799	TTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaThrA:   :::::::::   :::::::::   ::::::::::	486 2756
486 2755	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh	470 2706
2705	GCTGATTGAACTCCTGGATTCAGATAGGCAGGAACATCAAGATTTG	2656
469	rSerLeuLeuThrSerHisGluProGluGluValThrLys	453
453 2655	SPTOLYSTYrLysPhePheHisLysSerPheGlnGluTyrThrAlaGlyA:         :::    :::           :::	436 2606
436 2605	ValLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnArgPheLy	420 2556
419 2555	ysPheAspPheGluLeuGlnAspValSerSerValAsnGluAsp     :::   :::    ::   GCTTTGAGTTTAATGATGATGATCTCGCAGAAGCAGGGGTTGATGAAGAT	405 2506
405 2505	SCYSG1yAspLeuAlaLeuGluG1yValPheSerHisL       :::        :::     CTGTGGTGAGCTGGCCTTGAAAGGGTTTTTTTCATGTT	389 2456
388 2455	HisLysGlyValAlaAlaSerAspPheIleArg     :::::::::::::::::::::::::::::::	373 2424
372 2423	erHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 	356 2374
356 2373	eThrCysalaIleGlnMetGlyGluSerGluPheHisS        	339 2324
339 2323	/SLeuArgAsnLeuMetLysThrProLe     :::::::::             TTTGCAGAAGATACAGAAAACTCCTCT	323 2274
322 2273	GTCTGCGAAAGTTTATG	308 2224
308 2223	ralaGluValGlyAspMetThrGluAspSeralaGlnAlaL    ;;; 	291 2174
291 2173	VallleValThrThrThrThrGluCysLeuArgHisIleArgGlnPheGl::::::::::::::::::::::::::::::::::::	275 2124
274 2123	ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet	258 2079
· ~	TALITCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA	نا ۱

3747	UGJYASHLEULYSASHLEUTNILYSLEULIEMETASPASHLELYSMET.	3698
் 6 ம	aspLeuGlnAsnGlnArgLeuProGlyGlyaspLeuGlnAsnGlnArgLeuProGlyGlyll AATCCAGTCACAAGACCAAATCTTTCCTAAT	4 10
744 3653	luargHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis ::::::::::::::::::::::::::::::::::	729 3604
729 3603	.AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspG ::::::	713 3554
712 3553	CysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLys	697 3504
696 3503	euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg 	680 3454
680 3453	uValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL       :::::   ::::: ::::::::::::::::::	663 3404
663 3403	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl	647 3396
646 3395	hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer:::::::::::::::::::::::::::::::::::	631 3349
631 3348		626 3299
625 3298	GlyGlyAlaMetAlaSerTrpGlu	618 3249
617 3248	roasncysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr:::	603 3199
603 3198	PhePheGluHisLeuP	598 3149
597 3148	TyrLeuPheAsp	594 3099
593 3098	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIleProAsp     :::     ::::::    ::::::::::::::::	577 3052
577 3051	TyrGlnGluSerThrSerLysSerAlaLeuSerGlnGluPheGluA       :::::    	562 3005
561 3004	AsnSerPheValGluCysGlyIleHisLeu	552 2955
551 2954	ThrThrGluGlnGluIleLeuLysAlaIleAsnIle ::: :::::::::::::::::::::::::::::::::	540 2905

SMA õ and

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seq_documentation_block:
ID AAT71263 standard; cDNA;
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A new neuronal apoptosis inhibitor protein (NAIP) cDNA clone (AAT71263) was isolated from a human foetal spinal cord cDNA library by probing with the genomic insert in cosmid 25086, containing a CATT locus. An additional coding sequence (AAT71264), including exon 14a (see also AAT71265 and AAT71266), was subsequently obtd. The NAIP DNA sequence including exon 14a appears to be a predominant gene isoform which is not deleted or mutated in spinal muscular atrophy (SMA) patients. The NAIP gene was mapped to 5q13.1. NAIP (see also AAW20032 and AAW20033) is a negative regulator
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                                                                                                                                                                                                                                                                                        New neuronal inhibitor treating, e.g. cancer,
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                                                                                                                                                                                                                                           Example 4; Fig 5A-L; 102pp; English.
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AACCTGGAAGAATTGATCCTTCCTACTGGGGATGGAAT
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                                                                                                                                                                                                                                                                                     of apoptosis - useful for diagnosing AIDS or amyotrophic lateral sclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                             Robertson
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CTTATTCCTTTTAGATGACTACAAAGAAATATGTTCAATCCCTCAA....
                                                                                                                                                                                                                                                                                                                           ACTCTGTCATGTGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTC
                            lLeuPheLeuLeuAspGlyTyrAsnGluPhe....LysProGlnAsnC
                                                                                                                                                             lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr
                                                                                                                                                                                             CAGGTTCCAGCTGGTTTTCTACCTCTCCCTTAGTTCCACCAGACCAGACG
                                                                                                                                                                                                                rLysPheLysPheValPhePheLeuArgLeuSer.....ArgAlaGlnG
::::|||::::ArgAlaGlnG
                                                                                                                                                                                                                                                              CTGAAGAAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCTGTTAAA
                                                                                                                                                                                                                                                                               LeuGlnArgIleAlaMetLeuTrpGlySerGlyLySCySLySAlaLeuTh
                                                                                                                                                                                                                                                                                                                                                         lnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeu
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                                                                  GTTACTGAAATGTGCATGAGGAACATTATCCAGCAGTTAAAGAATCAGGT
                                                                                             IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa
                                                                                                                               SHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG
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551	ThrThrGluGlnGluIleLeuLysAlaIle:AsnIle	540
2904	TTGGAGAATATATCTGAAAATGATGAC	28 75
539	GlnSerValLysAs	533
2854	AAAGAGTC	2847
533	lnGluS	517
00 H	GGCCCAAAATTGTGTCTCATTTGCTCCATTTAGTGGATAAC	0
16	laValMetLysHisLeuAlaAlaValTyrGlnHisG	50
7		Ç
503	TyrSerSerLeuLeuArqTyrThrCysGlySerSerValGluAlaTh	486
486 2755	GlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleThrSerTh	470 2706
2705	GGCTGATTGAACTCCTGGATTCAGATAGGCAGGAAC	2656
469	ArgLeuSerSerLeuLeuThrSerHisGluProGluGl         :::	U
2655	CCATTCTACCGGTTTTTAAGTCCTGCCTTCCAAGAATTTCTTGCGG	2606
453	eHisLysSerPheGlnGluTyrThrAlaGl · · · · · ·	436
6 0	AAGATCTAACCATGTGCTTGATGAGCAAATTTACAGCCCAGAGAC	US I
ω	lLeuLeuThrThrGlvLeuLeuCvsLvsTvrThrAlaGlnArgPhe	420
419 2555	ysPheAspPheGluLeuGlnAspValSerSerValAsnGluAsp    :::   ::: :::   :::   SerSerValAsnGluAsp   SerSerValAsnGluAsp   SerSerValAsnGluAsp   SerSerValAsnGluAsp   SerSerValAsnGluAsp   SerSerValAsnGluAsp   SerSerValAsnGluAsp   SerSerValAsnGluAsp	405 2506
2505	AGCT	2456
405	erLeuAspHisCysGlyAspLeuAlaLeuGluGlyValPheSe	389
388 2455	sGly	373 2424
	ITTGATGATGTGCTTTTCAAGTCCTATATGGAACGCCTTTCCT	١ ،
7	SThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGl	ງ ຜ
2373	GTGGCGGCGATCTGTGCTCATTGGTT	2324
356	eValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHi	339
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339	leGlnLysSerArgCysLeuArgAsnLeuMetLysThrProI	323
N	CACATAATATGACTCGTCTGCGAAAGTT	2224
322	uIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLe	308
2223		2174
	${\tt AlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAla}$	291
	SCTGTCCGTACAAACAGGGCCAGGGACATCCGCCGATACC	2124
91	allleValThrThrThrGluCysLeuArgHisIleArgGlnPhe	275
2123		2079
274	luAlaLeuIleLysGluAsnHisArgPheLysA	258

nLeuLysLys 792 	snGluGluAspAlaIleLysLeuA	776
nIleLysMetA 776     :::::: TATAAATGTTT 3747	uGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAs ; ; ;        :::   ::: CCTGTGCCTGAAAGAACTGTCTGTGGATCTGGAGGGCAA	759 3698
ThrAspSerLe 759	ASpLeuGlnAsnGlnArgLeuProGlyGlyLeu :::    :::    :::    ACAATCCACTCACAAGACCAAATCTTTCCTAAT	745 3654
rIleHis 744 :::: AGTCTCAGGG 3653	luArgHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis ::::: ::::::::::::::::::::::::::::	729 3604
nrIleGluAspG 729 :: :::: 3CGCAGCCGAAC 3603	.AsnIleTyrSerLeuMetValGluAlaSerProLeuTl !!!: CTCTGTCACCAAGTGCTCCATAAGCAAGTTGGAACTCA	713 3554
ThrCysLys 712     CTGTCTAAGGC 3553	CysAlaGlyValAlaGlySerLeuSerLeuValLeuSer 	697 3504
euGlnIleLysArg 696   :::::::::::  TCCATTTAAACCAC 3503	euGlyLysIlePheSerSerAlaThrSerLeuArgL 	680 3454
ASPILETHRTYRL 680 ::: ATGCTTGAGATTC 3453	uValThrLeuArgAspPheSerLysLeuAsnLysGlnAs	663 3404
luPheArgThrLeuGl 663       TGTCTAGA 3403	ArgAlaValSerLeuPhePheAsnTrpLysGlnG	647 3396
CIleProSer 646	hrG1yG1yI1eHisMetG1uG1uA1aProG1uTh ::: ::: ::: ::: ::: ::: ::: ::: ::: :	631 · 3349
sAlaAlaGluAspT 631 :   :::     :GGCATCACCAGACC 3348	GGATAATGTAAAGAGCTATATGGATATGCAGCGCAC	626 3299
625 CTGAAAAAGA 3298	GlyGlyAlaMetAlaSerTrpGlu 	618 3249
uAspPheTyr 617    ::: GGACTATGCT 3248	roAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr 	603 3199
GluHisLeuP 603 :::     TCAGTTCTGG 3198	CTCAATACGAGGAAATAAGACATCACCCAGAGCACATTTTTCAGTTCTGG	598 3149
597 GCATCCACTT 3148	TyrLeuPheAsp	594 3099
nIleProAsp 593  ::: :::  CTTACAG 3098	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIle     :::      ::::     AATTCCTTCAAGGGAGAACACTGACTTTGGGTGCGCTTAACTTA	577 3052
GluPheGluA 577 TTTGTTTTGC 3051	TyrGlnGluSerThrSerLysSerAlaLeuSerGinGluPheGlu        :::::      TGCTTATCAAAGCAACACTGTTGCTGCGTGTTCTCCATTTGTTTTG	562 3005
561 GCCCTGAAAAC 3004	AsnSerPheValGluCysGlyIleHisLeu	552 2955
TTGTCCACAA 2954	TTTCACTGCAGATGCAGTTACTTAGGGGATTGTGGCAAATTTGTCCACAA	2905

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856	AlaGlnAsnLeuHisAsnLeuValLysLeuSerIleLeuAspLeuSe 856	841
3844	AATGCCAATGCC	8839
840	824 luIleGlnLeuValSerCysCysLeuSerAlaAsnAlaValLysIleLeu 840	824
3838	3791 GAAATTATTGATCCAAATTTCAGCTGAGTATGATCCTTCCAAACTAGT 3838	1791
824	pTyrIleValLysSerLeuSerSerGluProCysAspLeuGluG	809
3790	TTCCACCATATGGA 3790	3777
809	MetCysLeuPheHisLeuThrHisLeuSerAspIleGlyGluGlyMetAs	793
3776	3748 TTTCAGTCATTCCTGAAGAATTTCCAAAC	3748

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_gss:AZ720059
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gb_gs:AQ624020
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Database length: 1077921985
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-Q-/cgn2_1/USPTQ_spcol/US9697089/runat_25032002_105137_11138/app_query.fasta_1.1097
-DB-EST -QEMT=fastap -SUFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-GGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.000 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US9697089_@CGN1_1_4971
-NCPU=6 -LCPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARR_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1
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AQ889169 HS_2161_B1_A01_T7C_CI1
AQ320928 RPCII1-93C_TV_RPCI-1
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AQ28386 RPCII1-78E13.TV_RPCI-1
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gb_est2:BF499764
gb_est2:BG684008
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                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: M13-21 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
Other_GSSs: CITBI-E1-2528J13.TR
Contact: Shaying Zhao, William
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                                                                                                                                                                                                                                                                                                                                                                                         Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K. Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
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                                                                      /organism="Homo sapiens"
/db_xref="taxon;9606"
/clone=15528J13"
/clone_lib="CITBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2:
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B1409867 602962204F1 NCI_CGA
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BG994334 PMO-HT1166-130201-0
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                                                                                      Email: ddunn@genetics.utah.edu
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Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 602)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ360053 602 bp DNA GSS 02-OCT-2000 1M0103H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0103H11 F, DNA sequence.
                                                                                                                                                                                                                Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                        University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                          quality sequence stop: 602
Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                           uTyrThrAlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProG 465
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||:::||||||||||||||
|GCATGAACGAGGACGTCCTGGTGACAATAGGGCTCCTCTGTAAGTACACA 438
                          isGlyCysLeuLeuGlyLeuSerIleAlaLysArgProLeuTrpArgGln 531
                                                                                                                               AspIleThrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSe 498
ACGGCAGCCTACAAGGACTTTCAGTCACCAAGAGGCCTCTCTGGAGGCAG
                                                                                                    CACAGAAGCAACCAGGGCGGTCATGAGGCACCTTGCAATGGTTTATCAGC
                                                                                                                                                                                                         GACATCACATCCCTATATGGCAATCTGCTCCTCTACACGTGTGGGTCGTC
                                                                                                                                                                                                                                                                                                            AGGAGGTGAGCAAAGGGAACAGCTACTTAAACAAAATGGTTTCCATCTCT
                                                                                                                                                                                                                                                                                                                                      luGluValThrLysGlyAsnGlyTyrLeuGlnLysMetValSerIleSer 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAGGTGTGTTCGCCCACAAATTTGATTTTGAACCCGAGCATGGGTCCA 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTTCAGGTGATTTTGCCAGGAGCCTAGACTACTGTGGAGACCTGGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was blunt end-repaired with T4 DNA polymerase and T4 polymclectide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DN/was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.481
92.821
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
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alignment_block:
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Percent Similarity:
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   902
                                                                                                                                 869 HisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaLeuMe
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                                                         tLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeuLysH 902
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isLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTrpArg 918
                                                                                                                 CATGAACTGATCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGAT 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
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AV719179 GLC Homo sapie
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AV719179.1 GI:10816331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="Adult"
/lab_host="SOLR"
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/clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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LOCUS AV656315
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                                                                                                                                                                                                                                                      Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV656315 GLC Homo sapiens cDNA clone GLCEQA10 AV656315
                                                                                                                                                                                                  Email: hanzg@chgc.sh.cn
This clone is available at C
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Zeguang H
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                                              /note="Vector: pBluescript sk(-); Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                               gb_est1:AI263294
                                             Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome //
Clone distribution: NCI-CGAP clone distribution

Clone distribution: NGI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL www-bio.llnl.gov/bbrp/image/image.html Insert Length: 2146 Std Error: 0.00 Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                    AI263294
AI263294.1 GI:3871497
                                                                                                                                                                                                                                                                                                                                               qx57b01.x1 NCI_CGAP_Pan1
                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                           Unpublished (1997)
                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                       Mammalia; Eutheria; Primates;
1 (bases 1 to 364)
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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seq_documentation_block:
LOCUS BG210375
DEFINITION RST29913 Athersys
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US-09-697-089-2 x AI263294/rev
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Ratio: 5.132
Percent Similarity: 100.000
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Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
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Location/Qualifiers
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 476)
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/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sa
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sa
/note="Organ: primer: Oligo d
/note="Oligo delta" size 1.72 kb. Life Technologies catalog
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/clone_lib="NCI_CGAP_Pan1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                           Euteleostomi;
                                               Smith, E.,
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alignment_block:
US-09-697-089-2 x BG210375
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                                                                                                                                                                                                                                                                                                             236 CCTTGGTGGGTGTATTTGAGAATCTTAAGCAATTAGTGTTTTTTGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 ThrAlaLeuMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    906 alProGlnLeuValLysLeuGlyLeuLysAsnTrpArgLeuThrAspThr 922
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                                                                                                                                                                                                                                           SerThrLysGluPheLeuProAspProAlaLeuValArgLysLeuSerGl 989
                                                                                                                                                         nValLeuSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpG 1006
                                                                    lnPheAspAspAspAspLeuSerValIleThrGlyAlaPheLysLeuVal 1022
                                                                                                                                                                                                                         AGTACTAAAGAATTTCTACCTGATCCAGCATTAGTCAGAAAACTTAGCCA
                                                                                                                                                                                                                                                                                                                               laPheMetGlyValPheGluAsnLeuLysGlnLeuValPhePheAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                        eGlnGlnLeuAsnLeuAlaGlyAsnArgValSerSerAspGlyTrpLeuA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCCCCAG.....TAGCTGGGATTACCGGTCCATGCCGCCACT..... 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGTTCTCTATTTGCTTCTCTGGATCTGAAGTGATTCTCCTGCCTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTGCAGTGCGTTCTTGGCTCACTCGCACCTCCGCTTCCTGGGATTC
                                                                                                                                  AGTGTTATCCAAGTTAACTTTTCTGCAAGAAGCTAGGCTTGTTGGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Scott J. Cain Athersys, Inc. 3201 Carnegie Ave, Clev Tel: 216 431 9900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activation of Gene Expression Nat. Biotechnol. 19 (5), 440 (2001) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Creation of Genome-wide Protein Expression Libraries using Random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

107 g 149 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475.50
3.962
78.947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to: 476
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KEYWORDS
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US-09-697-089-2 x AQ624020
                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
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LOCUS AQ624020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_gss:AQ624020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                    Align seg 1/1 to: AQ624020
                                                                                                                                                                                                                                                               Percent Similarity:
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675 nAspIleThrTyrLeuGlyLysIlePheSerSerAlaThrSerLeuArgL 692
                                                                                           659 PheArgThrLeuGluValThrLeuArgAspPheSerLysLeuAsnLysGl
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                                                                  5 TTCATGACTCTGGAGGTCACACTCCGGGATTTCAGCAAGTNGAATAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h GenetLos (lifo@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 954 row: F column: 24 Seq primer: SP6 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ624020 470 bp DNA GSS 16-JUN-1999 HS_5378_B2_C12_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=954 Col=24 Row=F, DNA sequence.
                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jwallace@u.washington.edu
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 470
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen d and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                             445.50
4.455
70.922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=954 COL=24 ROW=F"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                  107 g
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donor

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seq_documentation_block:
LOCUS AW337918
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                                                                                                                                                                                                                                  High quality sequence stop: 201.
                                                                                                                                                                                                                                                                                        Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Elisabeth Paiettà, Jonathan D. Licht, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 261)
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                                                                                                                                                                                                                                                                            Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
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                                                      /clone_lib="NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 rearrangement positive, includes myeloid blast crisis"
/lab_host="DH10B"
/note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Library constructed by Life Technologies."
                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2918853"
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                                                                                                                18 pooled CML cases, BCR/ABL
                                                                                                both chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hominidae;
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                                                                                              phase
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HS_2161_B1_A01_T7C CIT Approved Human Genomic Sperm Library
sapiens genomic clone Plate=2161 Col=1 Row=B, DNA sequence.
AQ889169
                                                                                                                                                        Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 2161 row: B column: 1
                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
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Location/Qualifiers
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Class: BAC ends
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l: jwallace@u.washington.edu
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/db_xref="taxon:9606"
/clone="Plate=2161 Col=1
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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and

seq\_name:

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255 742 205 725 155 709 105 692

DEFINITION

REFERENCE

TITLE AUTHORS

QURNAL

SOURCE KEYWORDS VERSION

ORGANISM

FEATURES

source

/sex="male"

/clone\_lib="CIT Approved Human Genomic Sperm Library

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seq_documentation_block:
LOCUS AQ320928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_gss:AQ320928
 Email: hbe@tigr.org

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fi
                                                                                                      Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD:
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                              Unpublished (1998)
Other_GSSs: RPCI11-93C9.TJ
                                                                                                                                                                                                                                              Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
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                                         Unpublished, Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: T7 Class: BAC ends.
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1 (bases 1 to 219)
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                  Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                   Unpublished (1998)
                                                                                                                                                                                                                                                                                                            AQ283886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to reverse of: AQ320928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:7535384"
/db_xref="taxon:9606"
/clone="RPCI-11"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298.00
4.656
86.486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 81.081
                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 t
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                                                  20850, USA
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KEYWORDS
SOURCE
ORGANISM
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US-09-697-089-2 x AQ283886
                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_gss:AQ112439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                          VERSION
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                                     TITLE
  JOURNAL
                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 TGTGTGCTTTGTTCACTTAAAAAAAAAT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  734 erValThrAsnLeuLysThrLeuSerIleHisAspLeuGlnAsnGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 CTGCCGGGT.....ATTGTTAATATCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         717 uMetValGluAlaSerProLeuThrIleGluAspGluArgHisIleThrS 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     701 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 CATGGTGGAAGCCAGTCCCCTGACCATAGAAGATGAGAGGCACATCACAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GCTGGAAGCCTTAGTCTGGTCCTCAGCACCTGTAAGAACATTTATTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sLeuIleMetAspAsnIleLysMetAsn 776
                                                                                                                                                                                                                                                                  AQ112439
AQ112439.1 GI:3484599
GSS.
                                                                                                                                                                                                                                                                                                                                                        AQ112439 630 bp DNA GSS 29-AUG-1998 CIT-HSP-2372C1.TR CIT-HSP Homo sapiens genomic clone 2372C1, DNA
                                                                                           1 (bases 1 to 630)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pieter de Jong (pieterédéjong med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:
                           Map Building
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       sequence.
Unpublished (1998)
                                               Use of a random human BAC
                                                                       Venter,J.C.
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
a 45 c 46 g 59 t
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81.579
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/db_xref="taxon:9606"
/clone="RPCI-11-78E13"
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Gaps: 1
Percent Identity: 72.368
                                            End Sequence Database for Sequence-Ready
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SOURCE
ORGANISM
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US-09-697-089-2 x AQ112439
COMMENT
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                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                          KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est2:BF903662
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                     MEDLINE
                                       JOURNAL
                                                                                     TITLE
                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  784 AlaGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHi 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      817 erGluProCysAspLeuGluGluIleGlnLeuValSerCysCys 831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 GCTGAAGGCCTGAAAAACCTGAAGAAGATGTGTTTATTTCATTTGACCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGAACCCTGTGACCTTGAAGAAATTCAATTAGTCTCCTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_GSSs: CIT-HSP-2372C1.TF
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                  namman, 251)

1 (bases 1 to 251)

1 (bases 1 to 251)

Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baila, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clones are available from end search page: http://www.tigr.org/tdb/hu Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                   BF903662 251 bp mRNA EST 18-JAN-2001 IL2-MT0180-181200-276-F03 MT0180 Homo sapiens cDNA, mRNA sequence.
Contact: Simpson A.J.G.
                                         Proc. Natl.
                                                           sequence tags
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             BF903662.1 GI:12295121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255.00
5.312
100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2372C1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .630
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                                           Acad. Sci. U.S.A.
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Percent Identity:
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                                         97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics (info@resgen.com). BAC
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100.000
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SOURCE
ORGANISM
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KEYWORDS
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LOCUS AZ614134
                                                                                                                                                                                                                                          seq_name: gb_gss:AZ614134
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                                                                                                                                                          DEFINITION
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                                                                                                                                                                                                                                                                                                                                     402
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                                                                                                                                                                                                                                                                                                              heSerHisLysPheAspPheGluLeuGlnAspVal 413
                                                                                                                                                                                                                                                                                                                                                                                                     ACCCCTCTCTTTGAGGTCATCATTTGTGCAATCTCTATGGACAGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                              GACTCATTCGGAGCCTGACCACTGTGG.GACCTAGATCTGGTGGGTGCGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGATACAGAAAAACAAACACAAACATAAAGGCGTG.....TCTGATGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                luPheHisSerHisThrGlnThrThrLeuPheHisThrPheTyrAspLeu 369
                                                                                                                                                                                                                                                                                        TCTGCCACAAGTTTGAATTCGAACTGCAGGATGTG 230
                                                                                                                                 1M0442N17R Mouse 10kb plasmid UUGC1M library Mus clone UUGC1M0442N17 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0180-
181200-276-F03&t3=2000-12-18&t4=1)
                                                                                        AZ614134.1 GI:11736324
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                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: puc 18 forward
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                             house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Cancer Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 62 c 56 g 61 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248.50
3.883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MT0180"
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  358
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                                                                                           341 lValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisSerHisT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNT
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hrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGlnLysAsn 374
                                               GGCAGCAGTATGTACTGACTGGTTTGAAAATCCATCTGACCAGCCCTTTC 518
                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 625.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired
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and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 625)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwo42 (gil473214/gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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a 143 c 144 g 167 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                          244.00
1.952
66.489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="UUGC1M0442N17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGTTTTTAGGTCCGCTGTTCCAGGAGTTTCTTGCTGCCATGAGACTGA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rLysPhePheHisLysSerPheGinGluTyrThrAlaGlyArgArgLeuS 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAATAGTGATGACCTGGCAGAGGCAGGAGTTGATGAAGATGAAGAGCTC
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                                                                                                                                                            cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 509)
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EST.
                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                 quality sequence stop: 461.
Location/Qualifiers
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/db_xref="taxon:9606"
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996 eLeuGlnGluAlaArgLeuValGlyTrpGlnPheAspAspAspAspLeuS 1013
                                                                                                                                                                                          508 GATCCAGCATTAGTCAGAAAACTTAGCCAAGTGTTATCCAAGTTAACTTT
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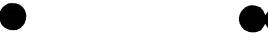
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Database sequences: 1472140
Database length: -341344837
Search time (sec): 1827.280000
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95 AY027789 Homo sapiens CLANE (CL
86 AY027789 Homo sapiens CLANE (CL
28 A64531 Sequence 23 from Patent
84 E23943 Excessive ovulatory ani
84 E24989 Apoptosis-inhibiting pr
24 IA64529 Sequence 2 from Patent
24 IU19251 Homo sapiens neuronal a
33 A64510 Sequence 2 from Patent
24 IU19251 Homo sapiens neuronal a
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25 IAF135494 Mus musculus clone 2
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29 A64509 Sequence 1 from Patent
29 A64501 Sequence 1 from patent
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TITLE
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Geddes, B.J., Wang, L., Huang, W.-J., Lavellee, M., N
Brown, M., Jurman, M., Morganstern, J., Merriam, S.,
DiStefano, P.S. and Bertin, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-APR-2001) Neurobiology, Inc., 640 Memorial Drive, Cambridge, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 284
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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i AF126484 Homo saptens CARD4
i AF113925 Homo saptens Nod1
i G55568 SHGC-100923 Human Hom
i AX082207 Sequence 9 from Pa
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Homo.
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alignment_block:
US-09-697-089-2 x AY032589
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267 uAsnHisArgPheLysAsnMetVallleValThrThrThrThrThrGluCysL
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                                                                                                 eTyrProLeuGlyGluAspIleAspIleIlePheAsnLeuLysSerThrP 134
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836	AAACCACCGCTTCAAGAACATGGTCATCGTCACCACTACCACTGAGTGCC 8	85
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301 936	ThrGluAspSerAlaGlnAlaLeuIleArgGluValLeuIleLysGluLe 3	17
317 986	uAlaGluGlyLeuLeuGlnIleGlnLysSerArgCysLeuArgAsnL 3 	34
334 1036	euMetLysThrProLeuPheValValIleThrCysAlaIleGlnMetGly 3 	50
351 1086	GluSerGluPheHisSerHisThrGlnThrThrLeuPheHisThrPheTy 3	135
367 1136	rAspLeuLeuIleGlnLysAsnLysHisLysHisLysGlyValAlaAlaS 3	185
384 1186	erAspPheIleArgSerLeuAspHisCysGlyAspLeuAlaLeuGluGly 4 	235
401 1236	ValPheSerHisLysPheAspPheGluLeuGlnAspValSerSerValAs 4	17 285
417 1286	nGluAspValLeuLeuThrThrGlyLeuLeuCysLysTyrThrAlaGlnA 4 	34
434 1336	rgPheLysProLysTyrLysPhePheHisLysSerPheGlnGluTyrThr 4	50 385
451 1386	AlaGlyArgArgLeuSerSerLeuLeuThrSerHisGluProGluGluVa 4	67 435
467 1436	1ThrtysGlyAsnGlyTyrLeuGlnLysMetValSerIleSerAspIleT 4	84 485
484 1486	hrSerThrTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGlu 5 	535
501 1536	AlaThrargAlaValMetLysHisLeuAlaAlaValTyrGlnHisGlyCy 5	17 585
517 1586	SLEULEUGlyLeuSerIleAlaLySArgProLeuTrpArgGlnGluSerL 5	34 635
534 1636	euGlnSerValLysAsnThrThrGluGlnGluIleLeuLysAlaIleAsn 5 	50 685
551 1686	IleAsnSerPheValGluCysGlyIleHisLeuTyrGlnGluSerThrSe 5	67 735
567	rLysSerAlaLeuSerGlnGluPheGluAlaPhePheGlnGlyLysSerL 5	84 785



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                                          CAAATGCAGTGAAAATCCTAGCTCAGAATCTTCACAATTTGGTCAAACTG
                                                                                                                                           rGluProCysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerA
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KEYWORDS
SOURCE
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MEDLINE
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Homo sapiens ICE-protease activating
AY035391
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                                                                                                                                               Submitted (16-MAY-2001) Microbiology and Immunology, The Jefferson University, 233 S. 10th Street, Philadelphia,
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 3219)
                                                                                                                                                                              Direct Submission
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21359454
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yet,J.-L., Srinivasula,
                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
 /note="IPAF; CED4/, recruitment domain
                                /map="p21-22"
145. .3219
                                                                                                                    Location/Qualifiers
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CED4/Apaf-1 family member; domain containing protein"
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               caspase-associated
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complete cd
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alignment_block:
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Quality: 5275.00
Ratio: 5.156
Percent Similarity: 99.902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 snArgGluGluValAsnIleIleCysCysGluLysValGluGlnAspAla 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 934
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                                        167
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101 395

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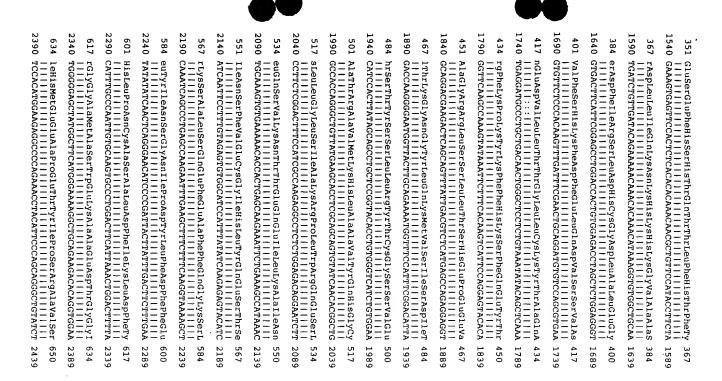
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ACCESSION VERSION KEYWORDS

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LOCUS AF376061 3581 bp mRNA PRI 15-MAY-2001
DEFINITION Homo sapiens caspase recruitment domain protein 12 mRNA, complete
cds.
ACCESSION AF376061
VERSION AF376061.1 GI:14040074

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JOURNAL
REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGIN
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Submitted (03-MAY-2001) Pediatric/Texas Children's Cancer Center,
Baylor College of Medicine, 6621 Fannin St. MC3-3320, Houston, TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gingras,M., Qiu,J. and Margolin,J.F.
Differential expression of the caspase recruitment domain protein
12 (CARD12) during monocytic differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 3581)
Gingras, M., Qiu, J. and Margolin, J.F.
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                                                                                                                                                                                                                                                                                                 to: 3581
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117 840	eTyrProLeuGlyGluAspIleAspIleIlePheAsnLeuLysSerThrP 1	34
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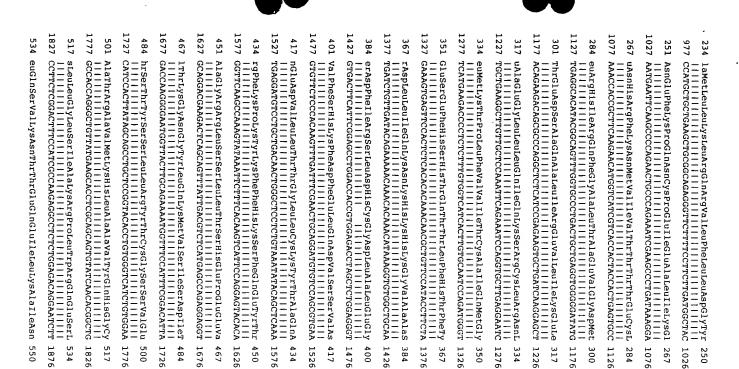


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3189		314
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3139		309
867 3089	1 SerileLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGluAl	85 304
850	4 laAsnAlaValLysTieLeuAlaGlnAsnLeuHisAsnLeuValLysLeu	83
3039		299
83 <b>4</b>	7 rGluProCysAspLeuGluGluIleGlnLeuValSerCysCysLeuSerA	81
2989		294
817	1 LeuSerAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSe	80
2939		289
800	4 laGluGlyLeuLysAsnLeuLysLysMetCysLeuPheHisLeuThrHis	78
2889		284
784	7 sLeulleMetAspAsnIleLysMetAsnGluGluAspAlaIleLysLeuA	76
2839		279
767 2789	1 LeuProGlyGlyLeuThrAspSerLeuGlyAsnLeuLysAsnLeuThrLy	75 274
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2739		269
734	7 uMetValGluAlaSerProLeuThrIleGluAspGluArgHisIleThrS	71
2689		264
717 2639	1 AlaGlySerLeuSerLeuValLeuSerThrCysLysAsnIleTyrSerLe	70 259
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684	7 gAspPheSerLysLeuAsnLysGlnAspIleThrTyrLeuGlyLysIleP	66
2539		249
667	1 LeuPhePheAsnTrpLysGlnGluPheArgThrLeuGluValThrLeuAr 	65 244

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MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL
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AUTHORS
TITLE
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ORGANISM
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Damiano, J.S., Stehlik, C., Pio, F., Ge Clan, a novel human ced-4-like gene Genomics. 75 (1-3), 77-83 (2001)
21365712
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Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Rd
Jolla, CA 92037, USA
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Homo sapiens CLANA (CLAN1) mRNA,
AYU27787
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Stehlik,C., Damiano,J.S., Pio,F., Godzik,A. and Reed,J.C.
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alignment_block:
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|TCACAGAACCTATCCTGTGGAGGAAGGACCAACACCATCACCGCGTGGAG
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                 sAspGlnLeuLeuAspIleProGlyThrIleArgLysGlnThrPheMetA
                                                                                                                                                             etLeuTrpGlySerGlyLysCysLysAlaLeuThrLysPheLysPheVal
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TGATCAACTCCTGGATATACCTGGCACAATCAGGAAGCAGACATTCATGG
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsnTr 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euMetLeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuLeu 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aLeuHisGluLeuIleAspArgMetAsnValLeuGluGlnLeuThrAlaL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAATGCAGTGAAAATCCTAGCTCAGAATCTTCACAATTTGGTCAAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          snProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTCATGAACTGATCGACAGGATGAACGTGCTAGAACAGCTCACCGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCTTTTAAACTAGTAACTGCT 3348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCTTGTTGGGTGGCAATTTGATGATGATGATCTCAGTGTTATTACAGG
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                                          Direct Submission
Submitted (28-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Aug 18, 2000 this sequence version replaced gi:8439959.
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 11 unordered pieces.
 Center: Washington University
                                                                                                                                    2 (bases 1 to 160583)
Waterston, R.H.
                                                                                                                                                                     The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                        1 (bases 1 to 160583) Waterston, R.H.
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                         AC010968.5 GI:9845170
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                              AC010968
                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                AC010968
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                     Genome Center
                                                                                                                                                                                                                                                                                                                                                                            DNA
2 c
                                                                                                                                                                                                                                                                                                                                                                              clone RP11-9302, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
   Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                            HTG
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                                                                                    Louis
                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                     misc_feature
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                 misc_teature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-primer ET; 47% of reads
Chemistry: Dye-terminator Big Dye; 53% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: bases at least Q40
Consensus quality: bases at least Q30
Consensus quality: bases at least Q20
Insert size: 147000; agarose-fp
Insert size: 159583; sum-of-contigs
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0093002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; 59%
Sequencing vector: plasmid; 41%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the configs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            17179
27159
27259
45138
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65523
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                                                                                                                                                                                                                                                                                                                                                                                                                                            116935: gap of unl
160583: contig of
                                                                                                                                                                                                                        .9606
                                                                                                                                                                                                                                                          .5035
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gap of unknown length
contig of 1296 bp in length
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g of 4471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 7372
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of 2459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 9980 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 25237 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
of 20285 bp in
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h length
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Spastin, a novel AAA protein, is altered in the most frequent of autosomal dominant spastic paraplegia
Nat. Genet. (1999) In press
2 (bases 1 to 138909) Submitted (29-FEB-2000) to the EMBL/GenBank/DDBJ databases On Mar 6, 2000 this sequence version replaced gi:6002386. Location/Qualifiers Direct Submission Genoscope. Artiguenave, F., Davoine, C.S., Cruaud, C., Durr, A., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Burgunder, J.M., Prud'Homme, J.F., Brice, A., Fontaine, B., Heilig, R. and Weissenbach 39243 a /organism="Homo sapiens" /db\_xref="taxon:9606" /chromosome="2" /clone\_lib="CITB\_978\_SKB" /clone="164M19" 28424 c 29121 g 42121 t .138909 Length: 1067
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74		74688
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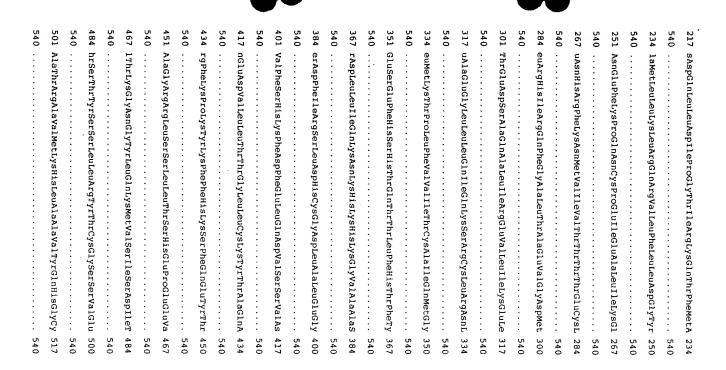
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNRS UPR 420 - Genetique Moleculaire et Biologie du Developement IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8 94801 Villejuif Cedex, FRANCE Tel: ++33-1-49 58 34 98 Fax: ++33-1-49 58 35 09 e-mail: auffray@infobiogen.fr
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The European IMAGE consortium for integrated Molecular analysis
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Damiano, J.S., Stehlik, C., Pio, F., Gc
Clan, a novel human ced-4-like gene
Genomics. 75 (1-3), 77-83 (2001)
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Stehlik,C., Damiano,J.S., Pio,F.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \verb"uValPhePheAspPheSerThrLysGluPheLeuProAspProAlaLeuV"
                                                                                                                                                                                                                                                                                                                                                                                                                                               snProLeuLysAsnPheGlnGlnLeuAsnLeuAlaGlyAsnArgValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAATGCAGTGAAAATCCTAGCTCAGAATCTTCACAATTTGGTCAAACTG
                                                                                                                                                                                                                                                                           yAlaPheLysLeuValThrAla 1024
                                                                                                                                                                                                                                                                                                                                                                                                   ## AGTGTTTTTTGACTTTAGTACTAAAGAATTTCTACCTGATCCAGCATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeu
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                                                                                                                                                                                                                                                                                                                     ArgLeuValGlyTrpGlnPheAspAspAspAspLeuSerValIleThrGl
                                                                                                                                                                                                                                                               TGCTTTTAAACTAGTAACTGCT
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2 (bases 1 to 768)
Stehlik,C., Damiano,J.S.,
Direct Submission
Submitted (21-FEB-2001) Pr
                                                                                                                                                                                   Homo sapiens CLANC AY027789
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 768)

Damiano,J.S., Stehlik,C., Pio,F., Godzik,A. and Reed,J.C. Clan, a novel human ced-4-like gene Genomics. 75 (1-3), 77-83 (2001)
                                                                                                                                      Homo sapiens
                                                                                                                                                                        AY027789.1 GI:14324116
                                                11472070
                                                                                                                                                                                 768 bp mkna
CLANC (CLAN1) mRNA, complete
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 Program
                      Pio, F., Godzik, A. and
 on
 Apoptosis
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                       Reed,J.C
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US-09-697-089-2 x AY027789
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727
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            151 GlnLeuThrLeu 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAsnPheIleLysAspAsnSerArgAlaLeuIleGlnArgMetGlyMe
                                                                      heThrGluProValLeuTrpArgLysAspGlnHisHisHisArgValGlu 150
                                                                                                                               eTyrProLeuGlyGluAspIleAspIleIlePheAsnLeuLysSerThrP
                                                                                                                                                                                                                                   nLeuPheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspL
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CAGCTGACCCTA
                                                                                                                 TTATCCCCTTGGTGAAGATATTGACATTATTTTAACTTGAAAAGCACCT
                                                                                                                                                                            TTGGCTCAGGATTTAAAGGACTTGTACCATACCCCATCTTTTCTGAACTT
                                                        TCACAGAACCTGTCCTGTGGAGGAAGGACCAACACCATCACCGCGTGGAG
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Ratio:
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Jolla, CA
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277...7
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1. .768
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738
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alignment_scores:
    Quality:
    Ratio:
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ACCESSION
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KEYWORDS
SOURCE
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AUTHORS
TITLE
JOURNAL
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US-09-697-089-2 x A64531
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LOCUS A64531
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                                                                                                                                                                                                                                                                                      1672 CCGATCTGGCCACGGACCACTTGCTGGGCTGTGATCTGTCTATT..... 1715
                                         1783 ACTCTGTCATGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTC
                                                                                                                                                                                                            1622 AGCTTATACCAGCGCCAGTTTCCGGCCACATGTCTTTGCTTGATATCTCTT 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1572 GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC 1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11:::|||
1522 TTGAAGATTCAATAGCAGTTGGTCCTATAGTGCCAGAAATGGCACAGGGT 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1472 GAGCCGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATC 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1425 TTTCTCCAAAATATGAAGTCC...TCTGCGGAAGTGACTCCAGACCTTCA 1471
                                                                 162 lnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeu 178 :::||| :::|||
                                                                                                                                               145 sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
179 LeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTh 195
                                                                                                                                                                                                                                                                                                                                                                                                                      85 nGlyGln......SerLeuPheHisGlnThrSerGluGlyAspL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 PheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspLeuAs
                                                                                                                                                                                                                                              AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi 145
                                                                                                                                                                                                                                                                                                                      .....TyrProLeuGlyGluAspIleAspIleIlePhe 128
                                                                                                                       .....CAAGAACCTCTGGTGCTGCCTGAGGTCTTTGGCAACTTGA 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o228 bp DNA
Sequence 23 from Patent WO9726331.
A64531
A64531.1 GI:3717929
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Korneluk, R.G., Mackenzie, A.E., Roy, N., Robertson, G. and Tamai, K. USE OF NEURONAL APOPTOSIS INHIBITOR PROTEIN (NAIP)

Patent: WO 9726331-A 23 24-JUL-1997;
UNIV OTTAWA (CA)
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Location/Qualifiers
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1332 c 1307 g 1
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Percent Identity: 23.736
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405 2505	ysGlyAspL      :::  GTGGTGAGC	389 2456
388 2455	LysAsnLysHisLysHisLysGlyValAlaAlaSerAspPheIleArg	373 2424
372 2423	erHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln	356 2374
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258 2078	lLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnC               	243 2033
243 2032	IleArgLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa::::::::::::::::::::::::::::::::::::	227 1983
226 · 1982	lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr        ::: :::            :::    ::: AGGGGCTGGCCAGTATCATCTGTGACCAGCTCCTAGAGAAAGAA	210 1933
210 1932	rLysPheLysPheValPhePheLeuArgLeuSerArgAlaGinG::::   ::::	195 1883
1882	CTGAAGAAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCTGTTAAA	1833

s 712    -   GGC 3553	CysAlaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLy	697 3504
Arg 696 ::: CAC 3503	euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLys 	680 3454
TYTL 680   	UValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrT      :::::   :::::::::::::::::::::::::	663 3404
uG1 663      AGA 3403	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuG	647 3396
Ser 646	hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProS ::: ::	a w
SpT 631    ACC 3348		626 3299
625 AGA 3298	GlyGlyAlaMetAlaSerTrpGlu	618 3249
Tyr 617 GCT 3248	roAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTy :::   :::      :::	603 3199
euP 603     TGG 3198	PhePheGluHisLeu	598 3149
597 CTT 3148	TyrLeuPheAsp	594 3099
Asp 593 ::: CAG 3098	laPhePheGlnGlyLysSerLeuTyrIleAsnSerGlyAsnIlePro    :::     :::      ATTCCTTCAAGGGAGAACACTGACTTTGGGTGCGCTTAACTTA	577 3052
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Gly 516 2846	rgAlaValMetLysHisLeuAlaAlaValTyrGlnHis :::    ::::     AGCAGGGCCCAAAATTGTGTCTCATTTGCTCCATTTAGTGGATAAC	503 2800
ThrA 503	rTyrSerSerLeuLeuArgTyrThrCysGlySerSerValGluAlaTh :   ::::::   :::   :::   CTACAACAATTTTTTGAACTATGTCTCCAGCCTCCAAC	486

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775		775
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787 3848	uLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuS ::::            TCAAAAFTCTCCAAACTTTAGCATCTGAAGTGTAACTTCTTTT TCAAAAFTCTCAAACTTCATGTTTGCATCTGAAGTGTAACTTCTTTTT	802 3897
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3898		3932
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834 3975	aAsnAlaValLysIleLeuAlaGlnAsnLeuHisAsnLeuValLysLeuS :::       ::::::    :::         :CAAGCCGTCCCATTTGTTGCCAGTTTGCCAAATTTTATTTCTCTGA	851 4020
851	erIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGlu::      ::::	66
4021	AAATUTTGAAGGUUAGCAATTTUUTGATGAGGAAACATUAGAA	40/0
867 4071	AlaieuHisGluteuIleAspArgMetAsnValLeuGluGlnLeuThrAl	883 4112
883	LeuProTrpGlyCysAspValGlnGlySerLeuSerSerLeuL	900
4113	GGAATTTATCGAGTGGCCAAACTGATCA	4161
900	euLysHisLeuGluGluValProGlnLeuValLysLeuGlyLeuLysAsn	916
2		,
917 <b>4</b> 212	TrpArgLeuThrAspThrGluIleArgIleLeuGl	928 4261
928 4262	yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuA  :::    	945 4293
945 4294	<pre>spGlyTrpLeuAlaPheMetGlyVal ::   :::      ::: aAGGATACAGAAATTTCTTTCAAGCA</pre>	960 4343
96	Th	J -7
4344	ATGCCAAACTTGCAGGAGTTGGACATCTCCAGGCATTTCAC	4393

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REFERENCE
AUTHORS
TITLE
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EFINITION
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Ratio:
Percent Similarity:
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cus E23943
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                                                                    1418
                                                                                                                                                                                       1368 GAGCCGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATC 1417
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                                                                                                                               98
                                                                                                                                                                                                                           85 nGlyGln......SerLeuPheHisGlnThrSerGluGlyAspL 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.

ISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

If (bases 1 to 5984)

If (bases 1 to 5984)

Shigehiro, I.K.M.M. and Sakai, H.O.

Excessive ovulatory animal and excessive ovulation method

Excessive ovulatory animal and excessive ovulation method

AL Patent: JP 1999113444-A 1 27-APR-1999;

SCIENCE & TECH ACENCY, HARUMI SAKAI

OS Homo sapiens (human)

PN JP 199911344-A/1

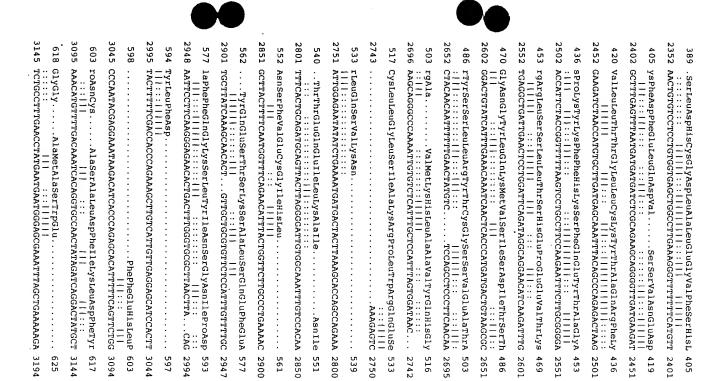
PD 27-APR-1999

PP 14-OCT-1997 JP 1997280830

PR SHIGEHIRO IKEDA, KAZUYA MATSUMOTO, HARUMI SAKAI, HITOSHI OSUGA PC

PATENTA ON TABLES ON CALANTE ON CALANTE OF COMMITTED COMMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PI SHIGEHIRO IKEDA, KAZUYA MATSUMOTO, HARUMI SAKAI, HITOSHI OSUGA PC A01K67/027, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC Strandedness: Double; CC Topology: Linear; FH Key Location/~~~~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E23943.1 GI 13024604
JP 1999113444-A/1.
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54.874
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Location/Qualifiers
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1267 c 1267 g 1673 t
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6
LeuAlaGlnAspLeuLysAs 107
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LysAsnLysHisLysGlyValAlaAlaSerAspPheIleArg 388 	373 LysAsnLysHisLysHisLysGlyValA :::	
erHisThrGlnThrThrLeuPheHisThrPheTyrAspLeuLeuIleGln 372    :::::::::   :::::::::::::::::::::::	356 erHisThrGlnThrThrLeuPheHisTh	
UPheValValIleThrCysAlaIleGlnMetGlyGluSerGluPheHisS 356        :::	339 uPheValVallleThrCysAlaIleGIn        ::  220 CTTTGTGGCCGGCGATCTGTGCTCATTGG	
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euIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu 322 :::::   ::::::::::::::::::::::::::::	308 euIleArgGluValLeuIleLysGluLe :::::   :::::::::::::::::::::::::::::	
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ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet 274	258 ysProGluIleGluAlaLeuIleLysGl 	
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lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr 226          :::                 AGGGGCTGGCCAGTATCATCTGTGACCAGCTCCTAGAGAAAAGAAGGATCT 1878	210 lyGlyLeuPheGluThrLeuCysAspGl         ::: :::           1829 AGGGGCTGGCCAGTATCATCTGTGACCA	
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TyrProLeuGlyGluAspIleAspIleIlePhe 128 :::	118TyrProLeuG1 :::        1568 CCGATCTGGCCACGGACCACTTGCTGGG	.=.
pLeuTyrHisThrProSerPheLeuAsnPhe	107 pLeuTyrHisThrProSerPheLeuAsn	_
GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC 1517	1468 GAAGCCCAGTGGTTTCAAGAGGCAAAGA	



900	alGlnGlySerLeuSerSerLeuL	883
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866 3966	erIleLeuAspLeuSerGluAsnTyrLeuGluLysAspGlyAsnGlu::       :::    ::       :::    AGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAGGAAACATCAGAA	851 3917
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802 3793	ThrHisLeuS ::: ::  AGTGTAACTTCTTTT	787 3744
787 3743	AsnGluGluAspAlaIleLysLeuAlaGluGlyLe	776 3694
ō,	TTTCAGTCATTCCTGAAGAATTTCCCAAACTTCCACCATATGGAGAAATTA	4 .
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696 3399	euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg    :::      :::::   ::::       :::::   TAATGACAGTTTTCTCAGCTTCACAGCGCATCGAACTCCATTTAAACCAC	680 3350
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4 4	CT : EH	
631 3244		626 . 3195

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BASE COUNT
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SOURCE
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LOCUS E24989
                                                                                                                                                                                        FEATURES
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AUTHORS
TITLE
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                                                                                                                                                     source
                                                                                                                                                                                                               Apoptosis-inhibiting protein, gene encoding the same and cDNA
Apoptosis-inhibiting protein, gene encoding the same and cDNA
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SCIENCE & TECH AGENCY
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PN JP 1993116599-A/1
PD 27-APR-1999
PF 14-OCT-1997 JP 1997280831
PR SHIGEHIRO IKEDA, KENJI YAMAMOTO
PC COTR14/52,COTK16/28,C12N15/09,C1201/68//C12P21/02,(C12P21/02
PC C12R1:19),
PC C12R1:19),
PC C12R1:19),
PC C12R1:19,
PC C
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5994)
Shigehiro, I. K. Y. Y.
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Apoptosis-inhibiting
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E24989.1 GI:13024687
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                                              1777
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C07K14/52,C07K16/28,C12N15/09,C12Q1/68//C12P21/02,(C12P21/02,
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Location/Qualifiers
1. .5984
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1267 c 1267 g 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA PAT protein, gene encoding
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lignment Percent	_scores: Quality: Ratio: Similarity:	653.00 1.074 54.874	Percent I	Length: 1108 Gaps: 42 dentity: 23.736	
alignment US-09-69	_block: )7-089-2 x E24	989	-1 ->:		
69 1321	PheLeuLysSei	uLysGlu :   ::: GAAGTCC	pAsnTyr ;;; .TCTGCG	roLeuPheGlnAspLeuA ;;: AAGTGACTCCAGACCTTC	.s 85 : A 1367
85 1368	nGlyGln :::::: GAGCCGTGGTGAAC	TŢ.	SerLeuPheHis :::   :::: TGTGAATTACTGGAA	isGlnThrSerGluGlyAspL 	L 98     C 1417
1418	euAspAsp				. 100
101			Leu	AlaGlnAspLeuLysA :::::   :::	s 107
107 1518	pLeuTyrHisThr     ::: AGCTTATACCAGC	ProSerPhe         GCCAGTTTC	LeuAsnPhe :::::::	CTTTGCTTGATATCTCTT	. 117 T 1567
118 1568	CCGATCTGGCCAC	TyrProLeuGlyG :::        GGACCACTTGCTGGGCT	oLeuGlyGl 	GluAspIleAspIleIlePhe     :::::    TGTGATCTGTCTATT	e 128 . 1611
129 1612	AsnLeuLysSerT ::::: GCTTCAAAAC	hrPheThr :::::: ACATCAGC	GluProValI :::       !AAACCTGTG.	.euTrpArgLysAspGlnH	i 145 . 1638
145 1639	sHisHisArgVal	alGluGlnLeuThrLeuAsnG        :::    AAGAACCTCTGGTGCTGCCTG	ThrLeuAsr :::    GTGCTGCC1	lyLeuLeuGlnAlaLeu ;;;;; H   AGGTCTTTGGCAACTTG	G 162 : A 1678
162 1679	<pre>lnSerProCysIl ::    ACTCTGTCATGTG</pre>	leIleGluGl :::      GTGTGGAGGG	yGluSer(     :::  TGAAGCT(	31yLysG1yLysSerThrLeu    :::      :::::     GAAGTGGAAAGACGGTCCTC	iu 178    C 1728
179 1729	LeuGlnArgIleA    :::::      CTGAAGAAAATAG	leAlaMetLeuT     :::      AGCTTTTCTGT	rpGlyserG   :::      GGGCATCTG	lyLysCysLysAlaLeuT 	h 195 : A 1778
195 1779	rLysPheLysPhe ::::   ::::: CAGGTTCCAGCTG	yalphephe       :::  GTTTTCTAC	LeuArgLe	uSerArgAlaGlnG            TAGTTCCACCAGACCAGACG	G 210 G 1828
210 1829	lyGlyLeuPheGlu        RGGGGCTGGCCAGT	ThrLeuCy :::   PATCATCTG	SASPGlnLeuLet            TGACCAGCTCCTI	uLeuAspIleProGlyThr     :::  CCTAGAGAAAGAAGGATCT	r 226 : T 1878
227 1879	IleArgLysGlnT ::: GTTACTGAAATGT	hrPheMetA ::: GCATGAGGA	tAlaMetLeuLeu :::::: GAACATTATCCAC	ıLysLeuArgGlnArgV :::   ::::::  ;CAGTTAAAGAATCAGG	'a 243    T 1928
243 1929	lLeuPheLeuLeuAspGl	AspGlyTyra:        :  GATGACTACA:	AsnGluPhe :::   ::: AAAGAAATATG	LysProGlnAsn        TCAATCCCTCAA	C 258 . 1974
258 1975	ysProGluIleGl     GTCATAGG	luAlaLeuIle         GAAAACTGATT	LysGl ::::: CAAAA	LSArgPheLySASnMe 	t 274 C 2019

275 ValileValThrThrThrGluCysLeuArgHisIleArgGlnPheGl 291

TGATGAT  LeuAsph  LeuAsph  LeuAsph  LeuSph  CGTGTCCT  GTGTCCT  TGAGTTT  TGAGTTT  TGAGTTT  TGAGTTT  IIII  TGAGTTT  TGAGTTT  IIII  TGAGTTT  IIII  TGAGTT  TGAGTT  TGAGTT  TGAGTT  TGAGTT  TGAGTT  TGAGTT  GTATCA  GTATCA  SerSerI  TGTATCA  AACAATT  AACAATT  AACAATT  AAGGGCCC  AGGGCCC  GuleuGl	TACTTTY TACTTTY TACTTTY IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	leArgG. :::   : TACGGAV  G1n:le G1n:le G1n:le TACGTTT
HisLysHisLy HisLysHisLy HisLysHisLy  PHISCYSGLY  CTCTTTGGTG  TTAATGATGAT  TLYSPHEPHEF                     ACCATGTGCTTTAA  CCGGTTTTAA  CCGGTTTTAA  CCGGTTTTAA  CTCTTCTAAACA  TYTLEUGLUCU  TYTLEUGINLY  CTTTTTGAACAC  TTTTTTGAACAC  TTTTTTTGAACAC  TTTTTTTGAACT  TTTTTTTGAACT  CAAAATTGTG  CCAAAATTGTGTG  SLYLEUSETI	TGGAAGACCAV TGGAAGAACCAV TGGAAGAACCAV TGGATCTGTGG  TGTTTTLEUI TGGCGATCTGTGG  TGTTTTGATGTGTGTGTGTGTGTGTGTGTGTGT	GluvalLeuI  AGCTCTTTC  BallleThrCys  GGAAAGAAC  AILLEThrLe  GGCGATCTGT  GGCGATCTGT  ShisLyshisl  AsphisCysdl  SHISLYSHISI  H  AsphisCysdl  SHISLYSHISI  AsphisCysdl  SHISLYSHISI  AsphisCysdl  SHISLYSHISI  AsphisCysdl  SHISLYSHISI  AsphisCysdl  SHISLYSHISI  AsphisCysdl  AsphisCysdl  AsphisCysdl  ATTTTAATGATG  SETSETLEULE  ATTTGAACTCC  YTYTLEUGINI  SETSETLEULE  ATTTGAACT  SETSETLEULE  ATTTGAACTCC  TCATTTGAAC  ATTTTTTTGAAC  ATTTTTTTTGAAC  ATTTTTTTTTGAAC  ATTTTTTTTTT
SCTGTTTCAAGT SHISLYSGLYVAL SHISLYSGLYVAL SHISLYSGLYVAL SHISLYSGLYVAL SHISLYSGLYVAL SHISLYSGLYVAL STGGTGAGCTGGG LEUGINASPVAL SATGATGATCATCTCC TGLYCATTAAGTCCTGG TITTAAGTCCTGGATTCAGG TELLEUThrSerF TITTAAGTCCTGGATTCAG TELLEUTHRSEFT TITTAAGTCCTGGATTCAG TELLEUTHRSEFT TITTAAGTCCTGGATTCAG TELLEUTHRSEFT TITTAAGTCCTGGATTCAG THE STGAACTATTCAG TAGACTATTCAG TAGACTAG TAGACTATTCAG TAGACTAG TAGACTAG TAGACTATTCAG TAGACTAG		/SGIULe :::::XTAATAT XYSLEMP //
TIGGCTGTTTCAAGTC  TGGCTGTTTTCAAGTC  LysH1sLysG1yValp  LysH1sLysG1yAspLeuAla	leThrCysAlaIleGlnM leThrCysAlaIleGlnM	ValleulleLysGluLeu :::::::::::::::::::::::::::::::::::
GATGTGCTTGATGAGTC  GATGTGCTGTTTTCAAGTC  SHISLYSHISLYSGIYVAIA  A	rGGAAGGARCCAAAGTTTGCA allleThrCysAlaIleGlnM :                 CGGCGATCTGGTGCTCATTGGT  Interpretation             CGCGATCTGTGCTCATTGGT  Interpretation           CATTON       C	SluValLeuIleLysGluLeu :::::::::::::::::::::::::::::::::::
ATGATGTGCTGTTTTCAAGTC LysHisLysHisLysGlyValA	rGGAAAGAACCAAAGTTTGCA alileThrCysalaileGlnm alileThrCysalaileGlnm cGGCGATCTGTGCTCATTGGT 3lnThrThrLeupheHisThr ccccattggraffCC 3ATGTGGCTGTTTTCAAGTCC 3HisLysHisLysGlyValai	31uValLeuIleLysGluLeu :::::::::::::::::::::::::::::::::::
	TGGAAGAACCAAAGTTTGCA TGGAAGACCAAAGTTTGCA  111eThrCysAlaIleGlnM :	SluValLeuIleLysGluLeu ::::::: AAGCTCTTTTCACATAATATG aGlnLysSerArgCysLeuAr    ::: rGGAAGAACCAAAGTTTGCA allleThrCysAlaIleGln ::       :: CGGCGATCTGTGCTCATTGGT

3743	ASIGNUCLUAS PALA LLELYS LEUA ASCUGLY VE	3694
6	TTCCTGAAGAATTTCCAAACTTCCACCATATGGAGAAATTA	4.
775		775
775 3643	uGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMet. : :                 ::::	759 3594
759 3593	ACAATCCAGTCACAAGACCAAATCTTCCTAATCTGGATAAGTT	745 3550
744 3549	luargHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis ::::::::::::::::::::::::::::::::::	729 3500
729 3499	.AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspg ::::::           :::           :::             :::	· 713
712 3449	CysalaGlyValAlaGlySerLeuSerLeuValLeuSerThrCysLys	697 3400
696 3399	euGlyLysIlePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg (	3350
680 3349	uValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL	663 3300
663 3299	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl	647 3292
	eHisMetGluGluAlaProGluThrTyrIleProSer ::: ::   ::	631
631 3244	LysalaalaGluaspT ( GGATAATGTAAAGAGCTATATGGATATGCAGCGCAGGGCATCACCAGACC )	626 3195
625 3194	GlyGlyAlaMetAlaSerTrpGlu	618 3145
617 3144	roAsnCysAlaSerAlaLeuAspPheIleLysLeuAspPheTyr	603 3095
603 3094	PhePheGluHisLeuP	598 3045
597 3044	TyrLeuPheAsp	594 2995
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577 2947	TGCTTATCAAAGCAACACTGTTGCTGCGTGTTCTCCATTTTGC	562 2901

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KEYWORDS
SOURCE
ORGANISM
                                                                                                      ACCESSION
VERSION
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LOCUS A64529
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yAlaPhePheGlyLysAsnProLeuLysAsnPheGlnGlnLeuAsnLeuA 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGATATTAAATCTTGAAGGCCAGCAATTTCCTGATGAGGAAACATCAGAA 3966
                                                                                                                                                                                                                                                                            GATGCAGATGATATTGCATTGCTT 4413
                                                                                                                                                                                                                                                                                                                       AspAspAspLeuSerValIle 1015
                                                                                                                                                                                                                                                                                                                                                                 TGTTACGACTACCAAGGCTCATTAGACTGAACATGTTAAGTTGGCTCTTG 4389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGACAACATGCCAAACTTGCAGGAGTTGGACATCTCCAGGCATTTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTTTGAATGATGACAGCGTGGTGGAAATTGCCAAAGTAGCAATCAGTGG 4157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCAGCAGTGTCAGCAGCTTCATTGTCTCCGAGTCCTCTCATTTTTCAAG 4107
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                                                                                                                                                                                                                                                                                                                                                                                                          euSerLysLeuThrPheLeuGlnGluAlaArgLeuValGlyTrpGlnPhe 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAGTGTATCAAAGCTCAGGCCACAACAGTCAAGTCTTTGAGTCAATGTG
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                                                                                                                             Sequence 21 from Patent A64529
                                        unidentified
                                                                                                         A64529.1 GI:3717928
                                                            unidentified.
                 unclassified
(bases 1 to 6124)
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1368 GAGCCGTGGTGAACTTTGTGAATTACTGGAAACCACAAGTGAAAGCAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 PheLeuLysSerLeuLysGluTrpAsnTyrProLeuPheGlnAspLeuAs 85
LeuGlnargIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTh 195
|||:::::||||||:::||||||:::|||||||
CTGAAGAAAATAGCTTTTCTGTGGGCATCTGGATGCTGTCCCCTGTTAAA 177
                                                                                                                                                                                                                                                                                            lnSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeu 178
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ACTCTGTCATGTGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTTATACCAGCGCCAGTTTCCGCCACATGTCTTTGCTTGATATCTCTT 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGCCCAGTGGTTTCAAGAGGCAAAGAATCTGAATGAGCAGCTGAGAGC 1517
                                                                                               lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr 226
                                                                                                                                      CAGGTTCCAGCTGGTTTTCTACCTCTCCCTTAGTTCCACCAGACCAGACG 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGATCTGGCCACGGACCACTTGCTGGGCTGTGATCTGTCTATT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....LeuAlaGlnAspLeuLysAs 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGAAGATTCAATAGCAGTTGGTCCTATAGTGCCAGAAATGGCACAGGGT 1467
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                                                                                                                                                                                                                                                                                                                                                                                                                sHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pLeuTyrHisThrProSerPheLeuAsnPhe.....
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Ratio:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIV OTTAWA (CA)
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Baird, S.D.
Direct Submission Submitted (24-NOV-1997) Stephen D. Baird, Children's Hospital of Eastern Ontario, Molecular Genetics, 401 Smyth Rd., Ottawa, Ontario, KlH 8L1, Canada Sequence of a 131-kb region of 5q13.1 muscular atrophy candidate genes SMN a Genomics 48 (1), 121-127 (1998) 2 (bases 1 to 6124) Chen,Q., Baird,S.D., Xuan,J.-Y., Kang,X., Roy, N., Mahadevan, M.S., McLean, M., Shutler, G., Yaraghi, Z., Farahini, R., Tamai, K., Ioannou, P., de Jong, P.J., Ikeda, J., Korneluk, R.G. and MacKenzie, A.
The gene for neuronal apoptosis inhibitory protein is partially deleted in individuals with spinal muscular atrophy Cell 80 (1), 167-178 (1995) Submitted (29-DEC-1994) Stephen D. Baird, Eastern Ontario, Molecular Genetics, 401 3 (bases 1 to 6124) Baird, S.D. Eastern Ontario, Molecular Ontario, K1H 8L1, Canada Direct Submission 98163755 MacKenzie, A.E. Mammalia; Eutheria; Primates; 1 (bases 1 to 6124) U19251.1 Homo sapiens neuronal apoptosis inhibitory protein mRNA, complete Eukaryota; Homo sapiens 5112344 24, 1997 this sequence version /number=3 289. .859 /product="neuronal apoptosis inhibitory protein"
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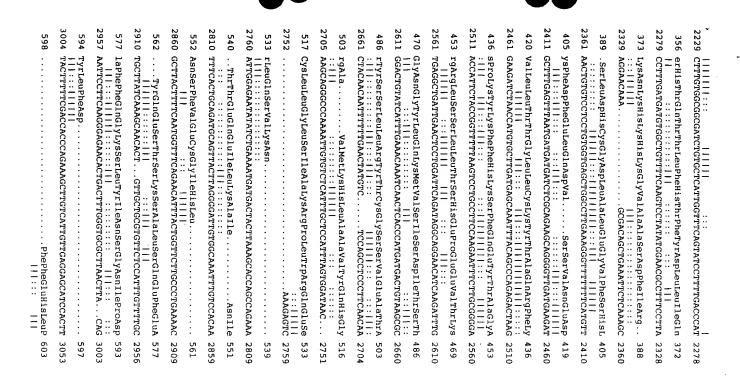
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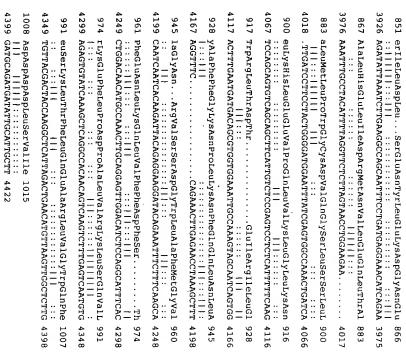
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LOCUS A64510
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                                                                                Align seg 1/1 to: A64510 from: 1 to: 6133
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EATURES
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4290
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Location/Qualifiers
1. 6133
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Sequence 2 from Patent W09726331.
A64510
A64510.1 GI:3717909
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Korneluk,R.G., Mackenzie,A.E., Roy,N., Robertson,G. and Tamai,K.
USE OF NEURONAL APOPTOSIS INHIBITOR PROTEIN (NAIP)
Patent: WO 9726331-A 2 24-JUL-1997;
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/db_xref="taxon:32644"
1299 c 1288 g 1740
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Gaps: 42
Percent Identity: 23.736
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95	IDheValValTleThrCvsAlaTleGlnMetGlvGlnSerGlnDheHisS	פני
339 2228	LeuGlnIleGlnLysSerArgCysLeuArgAsnLeuMetLysThrProLe	323 2179
322 2178	euIleArgGluValLeuIleLysGluLeuAlaGluGlyLeuLeu ::::   ::::::::::::::::::::::::::::::	308 2129
308 2128	yAlaLeuThrAlaGluValGlyAspMetThrGluAspSerAlaGlnAlaL     ::: agagaccatTcTagagaTcAaAagcaTTTcCcTTTTATAATACTGTcTGTA	291 2079
291 2078	ValileValThrThrThrThrGluCysLeuArgHisIleArgGlnPheGl::::::::::::::::::::::::::::::::::::	275 2029
274 2028	ysProGluIleGluAlaLeuIleLysGluAsnHisArgPheLysAsnMet          :::::      GTCATAGGAAAACTGATTCAAAAAAACCACTTATCCCGGACCTGC	258 1984
258 1983	lLeuPheLeuLeuAspGlyTyrAsnGluPheLysProGlnAsnC               	243 1938
243 1937	IleargLysGlnThrPheMetAlaMetLeuLeuLysLeuArgGlnArgVa ::::::::::::::::::::::::::::::::::::	227 1888
226 1887	lyGlyLeuPheGluThrLeuCysAspGlnLeuLeuAspIleProGlyThr        :::              :::    :::   aggggCTggCCAgTATCATCTGTGACCAGCTCCTAGAGAAAGAAGGATCT	210 1838
210 1837	rLysPheLysPheValPhePheLeuArgLeuSerArgAlaGlnG::::   ::::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::::	195 1788
195 1787	LeuGlnArgIleAlaMetLeuTrpGlySerGlyLysCysLysAlaLeuTh    :::::      :::      :::       	179 1738
178 1737	InSerProCysIleIleGluGlyGluSerGlyLysGlyLysSerThrLeu::    :::    ACTCTGTCATGTGTGTGGAGGGTGAAGCTGGAAGTGGAAAGACGGTCCTC	162 1688
162 1687	SHisHisArgValGluGlnLeuThrLeuAsnGlyLeuLeuGlnAlaLeuG	145 1648
145 1647	AsnLeuLysSerThrPheThrGluProValLeuTrpArgLysAspGlnHi ::::::::::::::::       GCTTCAAAACACATCAGCAAACCTGTG	129 1621
128 1620	TyrProLeuGlyGluAspIleAspIleIlePhe :::	118 1577
117 1576	PLeuTyrHisThrProSerPheLeuAsnPhe	107 1527
107 1526	LeuAlaGlnAspLeuLysAs	101 1477
100 1476	euAspAsp	98 1427
98 1426	nglyGlnSerLeuPheHisGlnThrSerGluglyAspL:::::::	1377



851 3925	AASHALAVALLYSILEEGUALAGINASHGEUHISASHGEUVALLYSIGUS :::       :::::    :::	834 3880
834 3879		819 3838
818 3837	erAspIleGlyGluGlyMetAspTyrIleValLysSerLeuSerSerGlu      :::   ::: 	802 3803
802 3802	uLysAsnLeuLysLysMetCysLeuPheHisLeuThrHisLeuS ::::    ::::    :::::   TCAAAATTCTCCAAACCTTCATGTTTTCCATCTGAAGTGTAACTTCTTTT	787 3753
787 3752	AsnGluGluAspAlaIleLysLeuAlaGluGlyLe	776 3703
3702	GAAGAATTTCCAAACTTCCACCATATGGAGAAATTA	3653
775		775
775 3652	uGlyAsnLeuLysAsnLeuThrLysLeuIleMetAspAsnIleLysMet. : :                 :::         ::::: CCTGTGCCTGAAAGAACTGTCTGTGGATCTGGAGGGCAATATAAATGTTT	759 3603
759 3602	AspLeuGlnAsnGlnArgLeuProGlyGlyLeuThrAspSerLe :::    :::   :::    :::    :::: ACAATCCAGTCACAAGACCAAATCTTTCCTAATCTGGATAAGTT	745 3559
744 3558	luargHisIleThrSerValThrAsnLeuLysThrLeuSerIleHis ::::::::::::::::::::::::::::::::::	729 3509
729 3508	.AsnIleTyrSerLeuMetValGluAlaSerProLeuThrIleGluAspG :::::	713 3459
712 3 <b>4</b> 58	ysLys     CTAAGGC	697 3409
696 3408	euGlyLys1lePheSerSerAlaThrSerLeuArgLeuGlnIleLysArg 	680 3359
680 3358	UValThrLeuArgAspPheSerLysLeuAsnLysGlnAspIleThrTyrL       :::::   ::::: ::::::::::::::::   AGTCGATGTGAATGATATTGATGTTGTAGGCCAGGATATGCTTGAGATTC	3309
663 3308	ArgAlaValSerLeuPhePheAsnTrpLysGlnGluPheArgThrLeuGl	647 3301
646 3300	hrGlyGlyIleHisMetGluGluAlaProGluThrTyrIleProSer::: ::	631 3254
N) (ii)		626 3204
625 3203	GlyGlyAlaMetAlaSerTrpGlu	618 3154
3153	TOASHCYSALASETALAUANSPERELELYSLAUASPEREYE :::	3104
3103	CCCAATACGAGGAAATAAGACATCACCCAGAGCACATTTTTCAGTTCTGG	3054



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Title:
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length: 2000000000
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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PCT-US96-12860-13
US-09-212-971-13
US-09-212-971-13
US-09-617-053A-13
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US-08-569-74-91
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US-08-344-596A-15
US-08-344-596A-15
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US-08-34-597-27
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US-08-569-749-13
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7271.527 Million cell updates/sec
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	ā-	- <del>a</del>	ccrctgrgatca               catctgtgacca	aattcgtctt             agctggtttt	tgctgcagcg          tcctgaagaa	DB 3; Le 3.5e-07; ches 115;		f Spinal A	hibitor			NTS	-353-585-1 -951-715A-6 -459-448A-6	754-4 791-1 791-4	755A~1 755A~4 754~1	320-8 088-1 585-4	439-2 439-7 320-3	664B-41 277A-41 439-1
	tca	agctgcggcagagggt1	arcaacrocrggar               accagotoctagag	gtottottoctocgtotcag	ctgcagcgcattgccatg              ctgaagaaaatagctttb	ength 5502 Indels		Muscular A	Protein, Ge				Seq Seq	s e g	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	s s s s s s s s s s s s s s s s s s s	s e c	ses ses ses
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: Sequence 13, Application PC/TUS9612860
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Matches 123; Conservative
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TELEPHONE: (415)781-1989
TELEPAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2862 base pairs
APPLICANT:
                                                                                                              2109
                                                                                                                                                                          2049
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                                                                                                                                                                                                                                   1989 CCGTTTTAGTCAAGGGAAATGCTGCAGCCAACATCTTCAAAAAACTCTCTGAAGGAAATTG
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
                                                                                                                               325 acttggacgatttggctcagga 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
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 TULARIK, INC
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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                                                                                              Sequence 13, Application Patent No. 6107041
                                                                               GENERAL INFORMATION:
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Best Local Similarity
                             APPLICANT: Korneluk,
APPLICANT: MacKenzie,
APPLICANT: Liston, Pe
    APPLICANT:
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                                                                                                                                                                                              2109
                                                                                                                                                                                                                                                            2049
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CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: A-
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REGISTRATION NUMBER: 2
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Baird, Stephen
Tsang, Benjamin
                                                 MacKenzie,
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06 AUG 1996
                                  Peter
                                                                Robert
                                                 Alexander
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; ORGANISM: Mus musculus
US-09-212-971-13
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Best Local Similarity
Matches 123; Conserv
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CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER FILING DATE: 1996-01-19
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 68/000,929
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER APPLICATION NUMBER: 08/800,929
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TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: WAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
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SOFTWARE: FastSEQ for
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               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                    APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
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CORRESPONDENCE ADDRESS
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cmreet: 176 Federal Street
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                                                                                   COUNTRY:
 OPERATING SYSTEM:
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                                                                                                                     Boston
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                                                                                                                                                                                                                                                                                                                        MacKenzie,
                                                                                                                                                                                                                                                                                                           Liston,
                                                                                                                                                                                                                                                                                                                                             Korneluk, Robert G
              IBM Compatible
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                                                                                                                                                                                                                                                                                                           Peter
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                                                                                                                                                                                                                                                                                                                         Alexander E
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Best Local Similarity 46.9
Matches 123; Conservative
               CURRENT APPLICATION NUMBER: US/09/617,053A CURRENT FILING DATE: 2000-07-14 PRIOR APPLICATION NUMBER: US 08/800,929 PRIOR FILING DATE: 1997-02-13
                                                                               TITLE OF INVENTION: DETECTION AND TITLE OF INVENTION: NAIP FOR THE TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009003
                                                                                                                                                                                                   APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexan
APPLICANT: Liston, Peter
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 NUMBER OF
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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SEQ ID NOS: 17
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Pratt, Christine
                                                                                                                                                                                                                    MacKenzie, Alexander
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APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION: CLASSIFFCHICATION DATA:
PRIOR APPLICATION NUMBER: 60/030,590 FastSEQ for Windows Version US/08/800,929A 07891/009001 2.0

Sequence 13, Application US/09617053A Patent No. 6300492 2175 TGACACATGTCCTTCCTATCCTGGATAATCTTCTTGAGGCCAGTGTAATTACAAAACAGG 85 tgactgttataaagcaaatcacagatgacctatttgtatggaatgttctgaatcgcgaag 144 actatcctctatttcaggacttgaatggacaaagtctttttcatcagacatcagaaggag ACGITICAGGCTTGTCATTGGA 2436 ACTCCACGTTATATGAAAACTTATTTGTGGAAAAGAATATGAAGTATATTCCAACAGAAG CCGTTTTAGTCAAGGGAAATGCTGCAGCCAACATCTTCAAAAACTCTCTGAAGGAAATTG Score 39.6; Pred. No. 0. Ħ MODULATION DIAGNOSIS / Mismatches DB 3; AND 139; TREATMENT OF IAPS AND Length 3151; Indels PROLIFERATIVE 0; Gaps 2354 264 2294 2234 2414 324 204

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ORGANISM: Mus musculus
US-09-617-053A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9505922A
GENERAL INFORMATION:
APPLICANT: HE, ET AL.
TITLE OF INVENTION: Human Inhibitor of Apoptosis Gene
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 123; Conserv
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SEQ ID NO 13
                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                INFORMATION FOR SEQ ID NO:
                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1435 BASE PAIRS
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5 INCH DISKETTE
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OPERATING SYSTEM:
               STRANDEDNESS:
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                                                                                                                                                                                                                                                                     CLASSIFICATION:
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TOPOLOGY:
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STATE: NEW JERSEY
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               NUCLEIC ACID
DEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 BECKER FARM ROAD
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                                                                                                   201-994-1744
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WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                      IBM PS/2
LINEAR
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CECCHI, STEWART & OLSTEIN
                                                                                                                                                                                                                                                                                  11 MAY 1995
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Pred. No. 0.17;
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RESULT 8
US-08-569-749-1
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Patent No. 6187557
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Best Local Similarity
Matches 122; Conserv
                                                                                                     TELEFAX: (415)398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111
COMPUTER READABLE FORM:
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MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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TOPOLOGY: lir
                                                                                                                                                                                         NAME: Brezner, David J. REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                  TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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                linear
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                              single
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er, Suite 3400
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Query Match Best Local Similarity

1.2%;

Score Pred.

36.8; No. 1;

DB 4;

Length 2589;

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                                                        Query Match 1.2%;
Best Local Similarity 46.2%;
Matches 122; Conservative
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                                                                                                                                                                                                                                          TELEFAX: (415)398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -US96-12860-1
 1607
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC'
FILING DATE: 06 AUG 19
                                                                                                                                                                                                                                                                       NAME: Brezner, David J.
REGISTION NUMBER: 24.774
REFERENCE/DOCKET NUMBER: A--
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1727
                                                                                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Brezner, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
COMPUTER: IF
                             83
                                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
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aatgactgttataaagcaaatcacagatgacctatttgtatggaatgttctgaatcgcga 142
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                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                  linear
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                                                                        Score 36.8;
Pred. No. 1;
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                                                          Mismatches 142;
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US-09-212-971-7
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LENGTH: 3532
TYPE: DNA
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Best Local Similarity 46.2%;
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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Pred. No. 1.
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Mismatches 142;
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Sequence 7, Application US/09212971B Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G

APPLICANT: MacKenzie,

Robert G , Alexander E

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Best Local Similarity
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EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
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TITLE OF INVENTION: I
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER READABLE FORM:
                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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compert: 176 Federal Street
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Pratt, Christine
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Baird, Stephen
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                                                                                                                              Clark & Elbing LLP
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                                                                                                                                                      APPLICANT: Korneluk, I
APPLICANT: MacKenzie
APPLICANT: Liston, Po
APPLICANT: Baird, St
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                                    TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009003
                                                                                                                  APPLICANT:
APPLICANT:
CURRENT APPLICATION NUMBER: US/09/617,053A CURRENT FILING DATE: 2000-07-14
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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Local Similarity 46.2%;
les 122; Conservative
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/017,354 FILING DATE: 26-APR-1996
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Pratt, Christine
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FastSEQ for Windows Version
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                                                                                                                                                        Stephen
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Pred. No. 1.3;
0; Mismatches 142;
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US-08-511-485-7
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Best Local Similarity 46.2%;
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                                                                 ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 075

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/800,929 PRIOR FILING DATE: 1997-02-13
                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3732
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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CLASSIFICATION: 514
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                                   TELEX:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C STREET: 225 Franklin Street
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                                                  617/542-8906
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Pred. No. 1.3;
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Best Local Similarity
Matches 121; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                 APPLICATION NUMBER: 07/973,341 FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                TELEPHONE: 312/474-6653
                                                                                                                                                      FILING DATE: 29-JAN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Materials and Methods NUMBER OF SEQUENCES: 59
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CITY: Chicago
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            TELEPHONE:
                                                                 NAME: Clough, David REGISTRATION NUMBER:
                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 09-NOV-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America
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                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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312/474-0448
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                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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                                                                                  David W
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Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           South Wacker Drive
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LOCATION: 57..1766
US-08-484-993B-15
Search completed: March 25, 2002, 11:39:43 Job time: 2967 sec
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SEQUENCE CHARACTERISTICS:
LENGTH: 1840 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Felis domesticus
DEVELOPMENTAL STAGE: Juvenile
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
CELL TYPE: Ovcyte
FFATURE:
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                                                                                                             1364 AGGGATCAGCTGGGTTTGATAG 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2900 tgccttcatgggtgtatttgag 2921
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                                                                                                                                                                                                                                                                                                                                                                                  1544 GGCAACAGGACAGGTTATCCTACAGGAGGAGGTCCCCAGCAGGCTGGCAGATGGATACATT 1485
                                                                                                                                                                                                     1424 GGTGAAAATACTGAAGCGCTTGTAGTAAGATGGAAATGGTGTATCCAGAGCCTTCTGGAC 1365
                                                                                                                                                                                                                                                                                             1484 ACAGTGCAGATACACCGGTCCCCTGAGTGCCCACTTTGCCATGGTGTCCACAAAGCTGAA 1425
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Maximum DB seq
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                                  3119.5
2980.6
1946.6
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242
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                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                        d. No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /SIDS2/gcgdata,
2: /SIDS2/gcgdata,
3: /SIDS2/gcgdata,
4: /SIDS2/gcgdata,
5: /SIDS2/gcgdata,
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length: 2000000000
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Match
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99.6
95.1
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/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT: *
/SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT: *
/SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT: *
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Listing first 45 summaries
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## ALIGNMENTS

AAS03945 RESULT Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway; cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; aplastic anaemia; myocardial infarction; inflammatory disorder; crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leprosy; tuberculosis; ischaemic brain injury; hypoxic brain injury; ss; kidney ischaemia; reperfusion injury; acute bacterial meningitis; excitatoxic brain damage; liver disease. WO200130971-A2 CDS Human caspase recruitment domain 12 (CARD-12) cDNA 12-SEP-2001 (first entry) AAS03945; AAS03945 standard; cDNA; 3133 Homo sapiens. -ب Location/Qualifiers 36..3110 /product= "Human CARD-12" /\*tag=

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crearitiment domain 12 (CARD-12) polypeptide. CARD domains are found in a
cumber of proteins that transmit signals that activate apoptosis and
inflammatory pathways in response to stress and other stimuli. Therefore,
CARD-12 and its corresponding nucleic acid may be used in treatment and
cd diagnosis of patients suffering from disorders associated with an
cd abnormal level (an increase or a decrease) of apoptotic cell death or
cd abnormal activity of stress-related pathways. The disorders include
cd cancer, viral infections (e.g. caused by poxviruses, adenoviruses),
cd autoimmune disorders (e.g. systemic lupus crythematosis, arthritis),
cd neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral
cd sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial
cd infarction, stroke), inflammatory and immune system disorders (e.g.
cd crohn's disease, insulin-dependent diabetes, contact dermatitis,
cd psoriasis, graft rejection), bacterial infections (e.g. tuberculosis,
cd ischaemia/reperfusion injury, excitotoxic brain damage, acute bacterial
cd meningitis and liver disease.
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Best Local Similarity 99.7
Matches 3124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA of the contraction
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                               gcagacattcatggccatgctgatgatgctgcggcagagggttcttttccttctttgatgg
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The sequence represents a genomic DNA which encodes the human caspase recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a number of proteins that transmit signals that activate appotosis and inflammatory pathways in response to stress and other stimuli. Therefore, CARD-12 and its corresponding nucleic acid may be used in treatment and diagnosis of patients suffering from disorders associated with an abnormal level (an increase or a decrease) of appototic cell death or abnormal activity of stress-related pathways. The disorders include cancer, viral infections (e.g. caused by poxviruses, adenoviruses),

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                                                                                                                                                                                                                                                                                                                 Isolated caspase recruitment domain-12 polypeptide and nucleic encoding them, useful for treating and diagnosing disorders assembly with abnormal apoptosis such as cancer, arthritis and Alzheimer disease
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WPI; 200 P-PSDB; 2001-457603/49 )B; AAM25640.

Isolated human and polynucleotides encoding diagnosis of e.g. cancer, polypeptides, uulcers and HIV useful for V infection the

Claim ۲. Page 511-512; 1217pp; English

antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoletic disorders, AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antiinheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antilcer; osteopathic; dermatological; antiallergic; antiasthmatic;

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                                                                                                                                 ttcatgggaaaaggctgcagaagacacaggtggaatccacatggaagaggccccagaaac 1960
                                                                                                                                                                                                                                                                                           catcgccaagaggcctctctggagacaggaatctttgcaaagtgtgaaaaacaccactga
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                                                                                                                                                                        gcccaattgtgcaagtgctctggacttcattaaactgggcttttatgggggagctatggc 720
                                                                                                                                                                                                                                  aagcttatatatcaactcagggaacatccccgattacttatttgacttctttgaacattt 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cagggctgttatgaagcacctcgcagcagtgtatcaacacggctgccttctcggactttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tcacaagtcattccaggagtacacagcaggacgaagactcagcagtttattgacgtctca
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                                                         ctacattcccagcagggctgtatctttgttcttcaactggaagcaggaattcaggactct
                                                                                                                   ttcatgggaaaaggctgcagaagacacaggtggaatccacatggaagaggccccagaaac
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99.8%;
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Pred. No. 0;
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, allergic
, depression,
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	1 aactgcttaaataaagtgtactcgaagccagta 3133 	310 192	Ф
3100	1 tgttgggtggcaatttgatgatgatgatctcagtgttattacaggtgcttttaaactagt	304	Qy
1920		186	Db
3040	1 attagtcagaaaacttagccaagtgttatccaagttaacttttctgcaagaagctaggct	298	Db Qy
1860		180	
2980	1 gaatottaagoaattagtgttttttgactttagtactaaagaatttctacctgatccagc	292	Qy
1800		174	Db
2920	1 gaatttggcgggaaatcgtgtgagcagtgatggatggcttgccttcatgggtgtatttga	286	Qy
1740		168	Db
2860	1 agagattagaattttaggtgcattttttggaaaagaaccctctgaaaaacttccagcagtt		Qу
1680			рь
2800	1 tttggaggaggtcccacaactcgtcaagcttgggttgaaaaactggagactcacagatac	274	Qy
1620		156	Db
2740	1 cgcactgatgctgccctggggctgtgacgtgcaaggcagcctgagcagcctgttgaaaca	268	Qy
1560		150	Db
2680	1 agatggaaatgaagctcttcatgaactgatcgacaggatgaacgtgctagaacagctcac	62	Qy
1500			Db
2620	1 gaatottoacaatttggtcaaactgagcattottgatttatcagaaaattacctggaaaa	256	Qу
1440		138	ДЬ
2560	1 tgaagaaattcaattagtc	250	Qy
1380		132	Db
2500	1 tgacattggagagggaatggattacatagtcaagtctctgtcaagtgaaccctgtgacct	4.4	Qy
1320		26	Db
2440	1 actagctgaaggcctgaaaa	20	Qy
1260			Db
2380	tacaaagctcataatggataacat	232	Qy
1200		114	Db
2320	1 tattcatgacctacagaatcaacggctgccgggtggtctgactga	226	Qy
1140		108	Db
2260	1) tcccctcaccatagaagatgagaggcacatcacatctgtaacaaacctgaaaaccttgag	220	Оу
1080		102	
2200	1 aagcetcagtttggtcetcagcacetgtaagaacatttattetetcatggtggaagecag	214	Qy
1020		96	Db
2140	1 aatattcagctctgccacaagcctcaggctgcaaataaagagatgtgctggtgtggctgg	208	Оу
960		90	

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AAH34171/c
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                                                                                                                                                                                                                                                                                                                                   CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon CC cancer-associated nucleic acid molecules (N) and proteins (P), where CC the proteins are collectively known as colon cancer antigens. The colon CC cancer antigens have cytostatic activity and can be used in gene CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders CC associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer-associated Ps, CC inactive proteins or to supplement the patients own production of P. CC Additionally, N may be used to produce the colon cancer-associated Ps, CC in a patient of colorectal cacidos into a host cell and culturing the cell CC by inserting the nucleic acids into a host cell and culturing the cell and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                       Matches
                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                   present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence 1 missing at time of publication, meaning no sequences SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding useful for preventing,
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                 2688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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03-NOV-1999;
                                                                                                                    2568 cacaatttggtcaaactgagcattcttgatttatcagaaaattacctggaaaaagatgga
                                                                                                                                                                                                                                                 Sequence 2735 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000; 2000WO-US26524
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atgctgccctggggctgtgacgtgcaaggcagcctgagcagcctgttgaaacatttggag
                                                              aatgaagctcttcatgaactgatcgacaggatgaacgtgctagaacagctcaccgcactg
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                                                                                                         CACAATTTGGTCAAACTGAGCATTCTTGATTTATCAGAAAATTACCTGGAAAAAGATGGA
                                              AATGAAGCTCTTCATGAACTGATCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTG
                                                                                                                                                                      al Similarity
565; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colon cancer; 
ctal carcinoma;
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99US-0163280.
                                                                                                                                                                                                                                                 791 A; 555
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diagnosing
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                                                                                                                                                                      0;
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                                                                                                                                                                   Score 564.4; DB 22;
Pred. No. 8.2e-156;
0; Mismatches 1;
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and/or treating colorectal
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tal cancers -
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                                              2608
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RESULT
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                              cervical cancer;
                                                                                                                                                                                                                                                                     Probe; human; microarray;
                                                                                                                                                                                                                                                                                        Probe
                                                                                                                                                                                                                                                                                                                           AAI14389;
                        Claim
                                                                                                     (MOLE-)
                                                                                                                                                                                          30-JAN-2001;
                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                         12-OCT-2001
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                                                                                    SG,
                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                              taaataaagtgtactcgaagccagta
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                                                                   2001-488901/53.
                        25;
                                       genome-derived single zing gene expression in
                                                                                                                                                                                                                                                                                        #4322
                                                                                                      MOLECULAR DYNAMICS
                      SEQ ID No 4322; 487pp; English.
                                                                                    Hanzel
                                                                                                                     2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234369
2000US-0236359
2000US-0236359
2000US-0236353
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                                                                                                                                                                                          2001WO-US00670
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                                                                                   DK,
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                                                                                   Chen
                                                                                                                                                                                                                                                                      gene expression; cervical epithelial cell;
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The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived

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RESULT
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Best Local S
Matches 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2996
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                       WPI; 2001-488897/53.
                                                                                                                      30-JUN-2000;
03-AUG-2000;
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26-MAY-2000;
                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                               genetic disorder;
                                                                                                                                                                                                                                                                         Probe; microarray;
                                                                                                                                                                                                                                                                                            Probe #4450 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2816 aggtgcattttttggaaagaaccctctgaaaaacttccagcagttgaatttggcgggaaa
                                                                                                21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                      WO200157272-A2
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                                                                                                                                                                                                                                                                                                                                                             AAI35764 standard;
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                                                                 (MOLE-)
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                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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0; Mismatches
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Best Local Similarity
Matches 242; Conserv
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                                                                                                       30-JUN-2000;
03-AUG-2000;
                                                                                                                             04-FEB-2000;
26-MAY-2000;
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27-SEP-2000;
                                                                                                                                                            29-JAN-2001;
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                                                                                                                                                                                                       WO200157270-A2
                                                                                                                                                                                                                                                           Probe; human;
                                                                                                                                                                                                                                                                              Probe #4204 used to measure gene expression
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                                                  MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                standard;
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                              Hanzel
                                                                                 2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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2000US-0207456
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                                                                        2000GB-0024263
                                                                                                                                                            2001WO-US00661
                                                                                                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                breast disease; breast cancer; development disorder; ss;
disease; proliferative breast disease; non-carcinoma tumour.
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                   Probe; human; microarray; gene expression;
cervical cancer; ss.
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                                                                       30-JAN-2001;
                                                                                               09-AUG-2001
                                                                                                                      WO200157278-A2
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                         Probe #13523
                                                                                                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                                                      AAI23590;
                                                                                                                                                                                                                                                                             AAI23590 standard;
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2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                        for gene expression analysis in human cervical cell sample
                                                                       2001WO-US00670
                                                                                                                                                                                                                               (first
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Pred. No. 4.4e-61;
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Matches
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exormicroarray, which can be used for measuring human gene expression in sample derived from human cervical epithelial cells. By measuring ger expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
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                                                                                                                                                                                   Probe #17590 used to
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04-OCT-2000;
                                                30-JAN-2001;
                                                                                                WO200157272-A2
                                                                                                                       Homo sapiens
                                                                                                                                                 genetic
                                                                                                                                                                                                            17-OCT-2001
                                                                                                                                                                                                                                                            AAI48904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
                                                                                                                                                                                                                                                                                                                                                                      gtcagaaaacttagccaagtgttatccaagttaacttttctgcaagaagctaggcttgtt 180
                                                                                                                                                                                                                                                                                                                                                                                                                        cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful
                                                                                                                                                microarray;
c disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID No 13523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene expression
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2000US-0180312.
2000US-0207456.
2000US-0608408.
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2000GB-0024263.
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                                                2001WO-US00663
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                                                                                                                                                  SS
                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;
                                                                                                                                                                                   measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quence is one such probe. The SENPs are derived The SENPs can be used to produce a single exon
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                                                                                                                                                          placenta;
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                                                                                                                                                                                                                                                             ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 220; DB
Pred. No. 9.1
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DR;
                                                                                                                                                             antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Т;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
9.1e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ring gene
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derived
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Best Local S
Matches 220
                                                                                                                                                                                                                                                                                  109206
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genc
analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                   Probe; human;
inflammatory (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                     09-AUG-2001
                                                                                                                          WO200157270-A2
                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                      Probe #9197 used
                                                                                                                                                                                                                            09-OCT-2001
                                                                                                                                                                                                                                                                        AAI09206 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 220
                                                                               29-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  gtcagaaaacttagccaagtgttatccaagttaacttttctgcaagaagctaggcttgtt 3044
                                                                                                                                                                                                                                                                                                                                                                                                                            Cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ttggcgggaaatcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaat
                                                                                                                                                                                                                                                                                                                                                                       gtcagaaaacttagccaagtgttatccaagttaacttttctgcaagaagctaggcttgtt
                                                                                                                                                                                                                                                                                                                                                                                                                 cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic ac
zing gene expression in human placenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No 17590; 654pp;
 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                      disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 58
                                                                               2001WO-US00661
                                                                                                                                                                                                                            (first
                                                                                                                                                                   breast disease; breast
disease; proliferative
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                                                                                                                                                                                                                                                                        DNA;
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100.0%;
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                                                                                                                                                                                                     gene
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Pred. No. 9.1e-55;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 G;
                                                                                                                                                                               breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                     expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                     t cancer; develo
breast disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid
nta –
                                                                                                                                                                                                     in human breast sample
                                                                                                                                                                               development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probes useful
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                                                                                                                                                                      non-carcinoma
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                                                                                                                                                                      tumour
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AAF58252/c
ID AAF582
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AC AAF582
AC AAF582
AC 24-APR
XX
Oligon
XW Electr
KW gene e
XX
Gene e
XX
Synthe
XX
WO2001
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PN WO2001
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PN 01-FEB
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PR 26-JUL
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PR 26-JUL
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the harset films of the proposition of the human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Electron-transfer group;
qene expression; ss.
                                                                                                                                                                      Oligonucleotide D1835
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                                                                                                                                                                                                                                                   AAF58252 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the breast, fibrocystic changes, proliferative non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000; 2000GB-0024263
 26-JUL-1999;
                           26-JUL-2000; 2000WO-US20476
                                                    01-FEB-2001
                                                                                                                                                                                                24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220;
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human breast -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                   DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 C;
                                                                                                                                                                                                                                                   936
                                                                                                                                            ETM; mismatch; genotyping;
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Pred. No. 9.1e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR;
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Best Local (
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  3001
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0.8%; Pred. No. 2.3e-17;
tive 461; Mismatches 31
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                     2401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer group, useful as labels hybridization assays, e.g. for genotyping, allowing repeat analyses a single surface -
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                                                                                                  936 BP; 4 A; 144 C;
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                     Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
Example 6;
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                                                                                                26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                       WO200107665-A2
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Page 127; 159pp; English
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Oligonucleotide 24-APR-2001

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h 3.0%; Score 94.8; DB 22; Length 936; Similarity 0.8%; Pred. No. 2.3e-17; 6; Conservative 461; Mismatches 313; Indels 0
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## ALIGNMENTS

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Unpublished (1998)
Other\_GSSs: CITBI-E1-2528J13.TR
Other\_GSSs: CITBI-E1-2528J13.TR
Contact: Shaying Zhao, William Nierman, Ma
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 208
Tel: 301 838 0208
Fax: 301 838 0208
Email: bbe@tigr.org end search page:
http://www.tigr.org/tdb/humgen/bac\_end\_search/bac\_end\_search.html.
Seq primer: M13-21
Class: BAC ends. Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and AQ309404 AQ309404 552 bp DNA GSS 22-DEC-1998 CITBI-E1-2528J13.TF CITBI-E1 Homo sapiens genomic clone 2528J13, Clones are availabe from Research Genetics (info@resgen.com). BAC Map Building Use of a random human BAC End Sequence Database for Venter,J.C. Eukaryota; Metazoa; Homo sapiens AQ309404.1 GI:4041438 DNA sequence. Mammalia; Eutheria; (bases 1 to 552) Location/Qualifiers
1. .552 /organism="Homo sapiens" Chordata; Primates; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. MD 20850 Mark Adams Sequence-Ready

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        Qian, B., Wu, T., Huang, Q., Huang, C., Kang, B., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Z., Y., Gu, Y., Chen, Z., and Han, Z.
                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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/clone="1528J13"
/clone=lib="CITBI-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: Ed CalTech Human BAC Library D"
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             wang, B., Gao, X., Xu
Nu, J., Song, H., Cheng, 2
, Ren, S., Zhong. M
                                                                                                                                                  GLCEQA10
                                                                            Vertebrata;
                                                                   Hominidae;
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                                                                             Euteleostomi;
                                           Xu, Z.,
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              1,Z.,
1,G.,
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                                Zeng,L.,
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                                           Xiao, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Zeguang Han
Contact: Zeguang Han
Chinese National Human Genome Center
351 Guo Shoujing Road, Zhangjiang H;
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                        GTGAGCAGTGATGGATGGCCTTGCCTTCATGGGTGTATTTGAGAATCTTAAGCAATTAGTG
                                                                                                                                                                                                                                                                                                                                                     GCATTTTTTGGAAAGAACCCTCTGAAAAACTTCCAGCAGTTGAATTTGGCGGGAAATCGT
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478; Conserv
                                              AZ360053
AZ360053.1
GSS.
Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                             AZ360053 602 bp DNA 1M0103H11F Mouse 10kb plasmid UUGC1M clone UUGC1M0103H11 F, DNA sequence.
                                     house mouse.
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clone is available at CHGC
Location/Qualifiers
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XhoI"
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/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="GLC"
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/db_xref="taxon:9606"
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  Chordata;
Rodentia;
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Pred. No. 5.8e
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Matches 478;
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                      | ataaattotttoacaagtoattocaggagtacacagcaggacgaagactcagcagtttat 1410
                                                                                                                                                                                         AAGGTGTGTTCGCCCACAAATTTGATTTTGAACCCGAGCATGGGTCCAGCATGAACGAGG
ATAAATTCTTTCATAAATCATTTCAGGAGTACACGGCAGGTCGGAGGACTCAGCAGTTTGC 356
                                                                                           ACGTCCTGGTGACAATAGGGCTCCTCTGTAAGTACACAGCTCAGAGGCTGAAGCCCACGT
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: H column: 11
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Rese
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114/gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0103H11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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2766 aagcttgggttgaaaaactggagactcacagatacagagattagaattttaggtgcattt 2825

Query Match 11.6%; Substitution 11.6%; Substitution 100.0%; Matches 364; Conservative 0;

Score 364; DB 10; Pred. No. 8.2e-86; 0; Mismatches 0;

Length 364; Indels

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BASE COUNT
ORIGIN
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE;2005417 mRNA sequence.
A1263294
                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                             High quality sequence stop: 364
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anal
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
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                       117
                                                                                                                                                                                                                                                                                                       primer: -40UP from Gibco
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                       þ
                                       /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
                                                                                                                                                                                                                                                1. .364
                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                       /lab_host="DH10B"
                                                                                                                                        /tissue_type="adenocarcinoma"
                                                                                                                                                             /clone_lib="NCI_CGAP_Pan1"
                                                                                                                                                                                /clone="IMAGE: 2005417"
                       84 c
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BASE COUNT
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Query Match
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Matches 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV656315 GLC
AV656315 GLC
AV656315
AV656315.1
                                                                                                                                                                                                                           Email: hanzg@chgc.sh.cn
This clone is available at C
Location/Qualifiers
                                                                                                                                                                                                                                                                   Contact: Zeguang Han
Chinese National Human Genome Cent
351 Guo Shoujing Road, Zhangjiang
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                    Xuau, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiac, Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Qu, J. Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., G., Yeng, Y., Ghen, Z. and Han, Z.
                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 371)
                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
               Similarity
                                                                                112
  Conservative
                                                                                                                                                                                                                                                                                                                                                               sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLC Homo sapiens cDNA clone GLCEQA10 3', mRNA sequence
                                                                                                                    /tissue_type="corresponding
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCEQA10"
                                                                                                          /note="Vector:
                                                                                                                                                              /clone_lib="GLC"
             11.1%;
98.6%;
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 0,
            Score 347;
Pred. No. 2.
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Zhangjiang Hi-Tech Park, Pudong,
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mes 5;
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RESULT
BG210375
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   Query Match 9.9%;
Best Local Similarity 97.8%;
Matches 313; Conservative
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Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                Activation of Gene Expression Nat. Biotechnol. 19 (5), 440 Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smi Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzi
                                                                                                                                                                                                                                                                                                                                                                                                                   Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Creation of Genome-wide Protein Expression Libraries using Random
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                           a
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Athersys
                                                                                                      /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

107 g 149 t l others
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contract Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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HS_5378_B2_C12_SP6E RPC
genomic clone Plate=954
                                                                                                                                                                                                        Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                           954 row: F column:
              /note-"Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one random! chosen donor and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the
                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=954 Col=24 Row=F"
                                                                       /sex="male"
                                                                                     /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                Location/Qualifiers
.6 vector at EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
AW337918
AW337918.1 GI:
                                                                                                                                                                                      Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                            Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D. Michael R. Emmert-Buck, M.D. Phona Library Preparation: 1 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, Th. Inc. A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                  www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP intp://www.ncbi.nlm.nih.gov/ncicgap.
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              /clone="IMAGE:2918853"
/clone_lib="NCI_CGAP_CML1"
/tissue_type="myeloid cells,
                                                      /db_xref="taxon:9606
                                                                      /organism="Homo sapiens"
                                                                                                            ocation/Qualifiers
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AQ889169/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ889169 404 bp DNA GSS 10-NOV-1999
HS_2161_B1_A01_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2161 Col=1 Row=B, DNA sequence.
                                                                                                               BAC end Web Server: http://www.htsc.washington.edu
Plate: 2161 row: B column: 1
                                                                                                                                        Clones may be purchased from Research Genetics (info@resgen.com)
                                                                                                                                                       401 Queen Anne Avenue North, Seat
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                 High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                           Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 404)
                                                                                                Seq primer: T7
                                                                                                                                                                                                                                                                                   scanning the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rearrangement positive, includes both chronic phase myeloid blast crisis" /lab_host="DH10B"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2161 Col=1
                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.1e-55;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aaaagggttcagagtcctgtaacctctttcttaaatccccttaaggagtggaactatcctc 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tcatttgctgcgagaaggtggagcaggatgctgctagaggggatcattcacatgattttga 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        taaagcaaatcacagatgacctatttgtatggaatgttctgaatcgcgaagaagtaaaca 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATTTTCTGGGAGAAGGTGGAGCAGGATGCTGTTAGAGGGATCATTCACATGATTTTGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ320928
AQ320928.1
GSS.
                                                                                                  Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                        Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
Other_GSSs: RPCI11-93C9.TJ
                                                                                                                                                                                                                                                                                                                                                         Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                        Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                        9712 Medical
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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RPCI11-93C9.TV
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E-Coli DH10B"
a 93 c 70 g
/organism="Homo sapiens"
/db_xref="GDB:7535384"
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/sex="male"
                                                    Location/Qualifiers
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91.2%;
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0; Mismatches 23
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/db\_xref="taxon:9606" /clone="RPCI-11-93C9" /clone\_lib="RPCI-11"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BF207840.1
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                                    276
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                                                                                                                 /tissue_type="carcinoma, cell line"
/lab host="DH10B (Tl phage-resistant)"
/lab host="DH10B (Tl phage-resistant)"
/lab host="Diadder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: pDNR-LIB (Clontech);
/note="Organ: bladder; vector: pDNR-LIB (Clontech);
/note="Organ: bladder; vecto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: Male BAC Library"
RPCIII Human Male BAC Library"
107 c 114 g 162 t
                                full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

143 c 165 g 256 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4082074"
/clone_lib="NIH_MGC_53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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3.7e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Chri: Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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Seg primer: -40UP from Gibco
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National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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ha21e11.x1 NCI_CGAP_Kid12 Homo sapiens
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                             /clone="IMAGE:2874380"
/clone_lib="NCI_CGAP_Kidl2"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DHIOB"
/lab_host="DHIOB"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-132831, 1471368-1472903 and
       1492104-1493255).
Fatima Bonaldo
                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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92.7%;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; E
1 (bases 1 to 219)
                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are darived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M.D., Rounsley, S.D., Zhao, S., Berry, K., Granger, D., Suh, E., Wible Use of human BAC End Sequences for
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RPCI11-78E13.TV RPCI-11
                                                                                                                                                                                                                                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
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                                  Similarity 86.
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Medical Center Dr., Rockville,
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                                                                                                                                                                                                                                                                                                                                         BAC ends.
                                                                                                                              /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
RPCI11 Human Male BAC Library"
45 c 46 g 59 t
                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="RPCI-11-78E13"
                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                       /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                       /db_xref="GDB:7529676"
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Primates;
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                                Score 157.2; DB 13
Pred. No. 8.1e-31;
D; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 162; DB 10;
Pred. No. 4.9e-32;
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                                                                 DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0180-
181200-276-F03&t3=2000-12-18&t4=1)
Seg primer: puc 18 forward
Seg primer: puc 18 forward
Utch Confidence of the confid
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
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as Neto,E., Garcia Correa,R., Verjovski-Almeida,S.,
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                                                                                                                                   /note="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
                          mRNA and cDNA amplification were performed under low stringency conditions." 62 c 56 g 61 t
                                                                                                                                                                                                                                                                                                                                                             /clone_lib="MT0180"
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Query Match Best Local S Matches 218

Local Similarity hes 218; Conser

Conservative

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Score 153.8; DB 11 Pred. No. 6.6e-30; 0; Mismatches 32;

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AQ112439
                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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CIT-HSP-2372C1.TR
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Other_GSSs: CIT-HSP-2372C1.TF
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Use of a random human BAC End Sequence Database for Sequence-Ready
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Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
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Search completed: March 25, 2002, 11:37:02 Job time: 2807 sec

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481	•	CDS
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Qy 361 accataccccatct                Db 361 ACCATACCCCATCT	Biophys. Res. Commun. 284 (1), 77-82 (2001) s 1 to 3133) T.	JOURNAL BIOChem. I PUBMED 11374873 REFERENCE 2 (bases AUTHORS Bertin, J.
	P.S. and Bertin, J. D12 Is a Novel CED4/Apaf-1 Family Member That Induc	TITLE Human Apopto
Db 241 TTCTTAAATCCCTT Oy 301 tttttcatcagaca	to 3133) , Wang,L., Huang,WJ., Lavellee,M., Manj: urman,M., Morganstern,J., Merriam,S., Gluo	REFERENCE 1 (bases 1 1 AUTHORS Geddes, B.J., Brown, M., Jul
Qy 241 ttcttaaatccctt	Metazoa utheria	-
Db 181 ATGCTGCTAGAGGG	3	KEYWORDS
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ا يُحَدُ	6 175086 2 AL157889 AL157889 HOMO 6 175213 2 CNS07EF6 AL512357 HOMO 6 175020 CNS07EF6 AL51237 HOMO 6 175020 AL512367 HOMO 6 175020 AL5123	200
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GDLALEGVFSHKFDFELQDVSSVNEDVLLTTGLLCKYTAQRFKPKYKFFHKSFQEYT
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  CTTCACAGAACCTGTCCTGTGGAGGAAGGACCAACACCATCACCGCG
                                                                                                                                   ttttctgaacttttatccccttggtgaagatattgacattattttta 420
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1860	ggaacarccccgartactrarrtgactctrcgacacttgcccaattgtgcaagtgctc [	1801	Db VY
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Poyet, J.-L., Srinivasula, S.M. Alnemri, E.S.
Direct Submission
Submitted (16-MAY-2001) Microfeferson University, 233 S.
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/product="ICE-protease activating factor"
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/db_xref="GI:14334215"
/fighthical="GI:1410"
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IFSSATSLRJGIKRCAGYAGSLSIVLSTCKNIYSLMVEASPLTIEDERHITSVUNLKT
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KNWRLTDTEIRILGAFFGKNPLKNFQQLNLAGNRVSSDGWLAFMGVFENLKQLVFFDF
STKEFLDPALVRKLSQVLSKLTFLQEARLVGWQFDDDDLSVITGAFFKLVTA*

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             Homo sapiens CLANA
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Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road,
Jolla, CA 92037, USA
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Stehlik,C., Damiano,J.S.,
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Clan, a novel human ced-4-like gene
Genomics. 75 (1-3), 77-83 (2001)
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1 (bases 1 to 3366)
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REFERENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANIS	SULT 376061 CUS FINITIO	b 331	ОУ 3072	Db 3253	Qy 3012	Db 3193	30 10	у 289	307	28	Db 3013	295	7	89		Qy 2592 Db 2833	Db 2773	Оу 2532	Db 2713	Qy 2472	65	241	Qy 2352 nh 2593	Db 2533	Оу 2292	Db 2473
alla; Eutheria; Primates; Catarrhini; Hominidae; Homo. bases 1 to 3581) ras,M., Qiu,J. and Margolin,J.F.	76061 76061.1 GI:14040074 an. o sapiens arvota: Metazoa: Chordata: Craniata: Vertebrata	AF37606 Homo sa	w	gtgttattacaggtgcttttaaactagtaactgcttaaataaa	AGTTAACTTTCTGCAAGAAGCTAGGCTTGTTGGGTGGCAATTTGATGATGATGATCTC 3312	agttaacttttctgcaagaagctaggcttgttgggtggcaatttgatgatgatga	aytat tadayaa t t t tadoo ay aa t tay cay aa taay tay tay baa aa ay ay t ta too ay ay t ta too ay ay ta too ay ay tay tay aa a	GATEGOTTE CONTRACTOR AND ANALYTICAL GATE AND CARTE AND C	gacttt 29	13	aqaaccctctqaaaaacttccaqcaqttqaatttqqcqqqaaatcqtqtqaqcaqtqat 28	yyyttyaaaaattyyayattaaayayattayaattitayyyytattettyi yotti liiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	AAGGCAGCCTGAGCAGCCTGTTGAAACATTTGGAGGAGGTCCCACAACTCGTCAAGCTT 30	caaggcagcctgagcagcctgttgaaacatttggaggaggtcccacaactcgtcaagctt 2771	Ū ⊦	יייי און אין אין אין אין אין אין אין אין אין אי	CTTGATTTATCAGAAAATTACCTGGAAAAAGATGGAAATGAAGCTCTTCATGAACTGATC 2892	TCTGCAAATGCAGTGAAAATCCTAGCTCAGAATCTTCACAATTTTGGTCAAACTGAGCATT 2832	ctgcaaatgcagtgaaaatcctagctcagaatcttcacaatttggtcaaactgagca	AAGTCTCTGTCAAGTGAACCCTGTGACCTTGAAGAAATTCAATTAGTCTCCTGCTGCTTG 2772	gtototgtoaagtgaacootgtgacottgaagaaattcaattagtotootgotgo	ATGTGTTTATTTCATTTGACCCACTTGTCTGACATTGGAGAGGGAATGGATTACATAGTC 2712	77	41	GTGGTCTGACTGACGTTGGGTAACTTGAAGAACCTTACAAAGCTCATAATGGATAA	ggtggtctgactgacagcttgggtaacttgaagaaccttacaaagctcataatggataac 2351	ACATCTGTAACAAACCTGAAAACCTTGAGTATTCATGACCTACAGAATCAACGGCTGCCG 2532

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Direct Submission
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Waterston, R. H.
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                               Center: Washington |
Center code: WUGSC
Web site:http://geno
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Submitted (28-SEP-1999) Genome Sequencing C
University School of Medicine, 4444 Forest
MO 63108, USA
On Aug 18, 2000 this sequence version repla
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HTG; HTGS
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Waterston, R.H.
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site:http://genome.wustl.edu/gsc/index.shtml
------- Project Information ------
iter project name: H_NH0093002
------ Summary Statistics -------
quencing vector: M13; 59%
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Insert size: 159583; sum-of-contigs
Quality coverage: 6.64 in Q20 bases; agarose-fp
Quality coverage: 6.38 in Q20 bases; sum-of-contigs
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AL389934
AL389934.1 G
FLI_CDNA.
                                                                                                                           http://www.iro.es e-mail enquirles: lsumoy@iro.es
EURO-IMAGE Consortium Contact: Auffray C
CNRS UPR 420 - Genetique Moleculaire et Biologie
IFR 1221 - Rue Guy Moquet 19, Batiment G - BP 8
94801 Villejuif Cedex, FRANCE
Tel: ++33-1-49 58 35 09
                                                                                                                                                                                                                             Recerca Oncologica (IRO), Hospital Duran i Reynals, Av. s/n Km 2,7 L'Hospitalet de Llobregat, 08907 Barcelona, (SPAIN. Tel: ++34-93-260-7775 Fax: ++34-93-260-7776 WWW:
                                                                                                                                                                                                                                                                   Pluvinet,R., Estivill,X., Esca
Direct Submission
Submitted (15-JUL-2000) Dept.
                                       IMPORTANT: This sequence represents the full insert of this IMAGE cDNA clone. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it
                                                                                                                                                                                                                                                                                                                                                                    Auffray, C., Ansorge, W., Ballabio, A., Estivill, X., Lehrach, H., Poustka, A. and Lundeberg, J.
                             corresponds was derived.
                                                                                     Distributors.
                                                                                               This clone is available royalty-free
                                                                                                               e-mail: auffray@infobiogen.fr
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LGNORLPGGLTDSLGNIKNLTKLIMDNIKMHEEDAIKLAEGLKNLKWCLFHLTHLSD
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ROGNEALHRELIDRMNVLEQLTALMLPMGCDVQGSLSSLLKHLEEFVPQLVKLGLKNWRL
TDTEIRILGAFFGKNPLKHOQLNLAGNRVSSDGWLAFMGVFENLKQLVFFDFSTKEF
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a 265 c 312 g 362 t
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musculus]
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AY027788
AY027788.1 G
                      2 (bases 1 to 1395)
Stehlik,C., Damiano,J.S., Pio,F., (
Direct Submission
Submitted (21-FEB-2001) Program on Research, The Burnham Institute, 11
Jolla, CA 92037, USA
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1395)
Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reec Clan, a novel human ced-4-like gene
Genomics: 75 (1-3), 77-83 (2001)
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/product="CLANB"

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/protein_id="AAR14777.1"

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LIMDNIKMNEEDDAIKLAEGLKRIKKNCLFHLTHLSDIGEGMDYIVKSLSSEPODLEIT
QLVSCCLSANAVKILAQNLHNLVKLSIIDLSENYLEKDGNEALHELIDRMNVLEQLTA
LMLPMGCDVGGSLSSLLKHLEEVPQLVVKLGLKWRLTDTEIRIIGAFFGKNPLKNFQQ
LNLAGNRVSBOGWLAFMGVFENKPLKVDLVFFDFSTKEFLPDPALVRKLSQVLSKLTFLQE
ARLVGMQFDDDDLSVITGAFKLVTA"
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/tissue_type="lung"
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/db_xref="taxon:9606"
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                                                                CAAAGAATGGGAATGACTGTTATAAAGCAAATCACAGATGACCTATTTGTATGGAATGTT
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Stehlik, C., Damiano
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Damiano,J.S., Stehlik,G., Pio,F., Godzik,A. and Reed,J.C. Clan, a novel human ced-4-like gene Genomics. 75 (1-3), 77-83 (2001)
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/product="CLANC"
/product="CLANC"
/protein_id="ARK14778.1"
/db_xref="GI:14324117"
/db_xref="GI:14324117"
/translation="MNFIKDUSRALIORNGMTVIKQITDDLFVMNVLNREEVNIICGE
KVEQDARGIIHMIKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGDLDDLA
KVEQDARFGIIHMIKKGSESCNLFIKSLKEWNYPLFQDLNGQSLFHQTSEGDLDDLA
QDLKDLYHTPSFLNFYEJGEDLDIIFNLKSTFTEPVLMRKDQHHHRVEQLTLYL"
a 157 c 180 g 213 t
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277. .747
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-FEB-2000) to the EMBL/GenBank/DE On Mar 6, 2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Hazan, J., Fonknechten, N., Mavel, D., Paternotte, C.,
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Mammalla; Eutheria; Primates;
1 (bases 1 to 185281)
Waterston, R.H.
                                   * as soon as it is available and the accession number will * be preserved.
                                                                 * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                             * NOTE: This is a 'working draft' sequence. It currently 
* consists of 7 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
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Waterston, R.H.
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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1985: contig of 1985 bp in 2085: gap of unknown length
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-78E13"
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112232: .185581
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7: contig of 27636 bp in 1
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Mammalia; Eutheria; I
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Stehlik,C., Damiano,J.S., Pio,F., Godzik,A.
Direct Submission
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Damiano, J.S., Stahlik, C., Pio, F., Godzik, A. and Reed, J.C. Clan, a novel human ced-4-like gene Genomics. 75 (1-3), 77-83 (2001)
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Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: olivier@shgc.stanford.edu
Primer A: AATAAGGGGGCAAAATAAGCAAA
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Fax: (650) 320-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Michael Olivier, David R. Cox
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olivier, M. and Cox, D.R. (2000) Unpublished, Olivier, M., Cox, D.R. (2000)
 AC010968.5 GI:9845170
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PCR Cycles:
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KCl:
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AmpliTaq Gold Polymerase:
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Human"
                                                               160583 bp
                                                                                                                                                                                                                                                                                                                                                  5.4%; Score 170; DB 11; 100.0%; Pred. No. 4.6e-80;
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                                             NA HTG 18-AUG-2000 Clone RP11-9302, WORKING DRAFT SEQUENCE,
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94 degrees
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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misc_feature
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Submitted (28-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of il contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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On Aug 18, 2000 this sequence version replaced gi:8439959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
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                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                              1. .160583
                                                                                            Location/Qualifiers
             /clone="RP11-9302"
                                                                                                    1080: contig of 1080 bp in length
2476: contig of 1296 bp in length
2576: gap of unknown length
2576: gap of unknown length
5035: contig of 2459 bp in length
5135: gap of unknown length
9606: contig of 2459 bp in length
9706: gap of unknown length
17078: contig of 7372 bp in length
17178: gap of unknown length
27158: contig of 9980 bp in length
27158: contig of 9980 bp in length
45137: contig of 17879 bp in length
45237: gap of unknown length
45237: gap of unknown length
45237: gap of unknown length
65622: gap of unknown length
65622: gap of unknown length
166352: contig of 25876 bp in length
116835: contig of 25377 bp in length
116835: contig of 35373 bp in length
116835: contig of 43648 bp in length
160583: contig of 43648 bp in length
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HOMO Sapiens chromosome 11 clone RP11-750A9, WORKING DRAFT SEQUENCE, 25 unordered pieces.
                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                  Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                         Direct Submission
Submitted (16-JUL-2000) Genome
University School of Medicine,
                                                                                                                                                                                                              2 (bases 1 to 175152) Waterston, R.H.
                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
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Mammalia; Eutheria; Primates;
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Aug 13,
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, 2000 this sequence version replaced gi:9743495
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116936: .160583
/note="assembly_name:Contig21"
. 33843 c 33703 g 47641 t
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1181. .2476
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17179. .27158
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91599. .116835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig13"
                                                                                                                                                                         (16-JUL-2000) Genome Sequencing Center, Washington School of Medicine, 4444 Forest Park Parkway, St.
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                                                                           Project Information
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.17078
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  /clone="RP11-750A9"
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                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                          /chromosome="]
                                                                       Location/Qualifiers
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                                      AC019059.4 GI:8567959
HTG; HTGS_PHASE1; HTGS_DRAFT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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94982. .104766
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74950. .83615
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3175. .5534
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132916. .148952
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Center project name: H_NH0125F14

Sequencing vector: M13; 70%
Sequencing vector: plasmid; 30%
Sequencing vector: plasmid; 30%
Chemistry: Dye-primer ET; 70% of reads
Chemistry: Dye-terminator Big Dye; 30% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 164779 bases at least Q30
Consensus quality: 174798 bases at least Q30
Consensus quality: 174798 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 167000; agarose-fp
Insert size: 180556; sum-of-contigs
Quality coverage: 3.76 in Q20 bases; agarose-fp
Quality coverage: 3.61 in Q20 bases; sum-of-contigs
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Web site:http://genome.wustl.edu/gsc/index.shtml
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On Jun 15,
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Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
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33727. .37341
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16285. .20536
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58281. .63165
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/db_xref="taxon:9606"
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DE 2 (bases 1 to 188459)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, L., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthaws, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Phunkhang, P., Pierre, N., Pollara, V., Rogov, P., Roman, J., Rosetti, M., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-125F14
Unpublished
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HOMO sapiens chromosome 11 clone RP11-125F14 map
SEQUENCE, 15 unordered pieces.
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Mammalia; Eutheria; Primates;
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167824. 183556
/note-"assembly_name:Contig37"
46765 c 45344 g 44562 t
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154241. .167723
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clone_end:T7
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/note="assembly_name:Contig26"
73942. .79919
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117254. .128332
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80020. .86721
/note="assembly_name:Contig28"
86822. .92876
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5671: contig of 5671 bp in length
5672 5771: gap of 100 bp
5772 5771: gap of 100 bp
5772 6377: contig of 606 bp in length
6378 6477: gap of 100 bp
6478 7122: contig of 645 bp in length
7123 7222: gap of 100 bp
7223 8771: contig of 1549 bp in length
8772 8871: gap of 100 bp
10767 10666: contig of 1795 bp in length
1067 10766: gap of 100 bp
10767 13839: contig of 3073 bp in length
13840 13939: gap of 100 bp
11767 13839: contig of 4087 bp in length
13907 18126: contig of 4087 bp in length
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90537 117488
117489 117588: 117589 145954
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Insert size: 187059; sum-of-contlys
Quality coverage: 8.4 in Q20 bases; agarose-fp
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
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69777 904:
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ation/Qualifiers
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174878: contig of 28824 bp in
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117488: contig of 26952 bp
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69676: contig of 37748 bp in
776: gap of 100 bp
90436: contig of 20660 bp in
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24163: contig of 6037 bp in length
263: gap of 100 bp
31828: contig of 7565 bp in length
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KEYWORDS
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AC090559
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson, Barna,N., Bastlen,V., Boguslavkly,L., Boukhgalter,B., Brown,A., Camparata,J., Campoplano,A., Choepel,Y., Colangelo,M., Collins,S. Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                                               Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-750H9
                                                                                                                                                                                                                                                          AC090559 204487 bp DNA HTG
Homo sapiens chromosome 11 clone RP11-750H9
SEQUENCE, 16 unordered pieces.
                                                                              Unpublished
                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 204487)
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69777, .90476
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8872. .10666
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5772. .6377
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174979. .188459
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146055. .174878
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90537. .117488
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24264. .31828
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1, .5671
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Submitted (03-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 11, 2001 this sequence version replaced gi:14150930. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Zembek,L., Zimmer,A. and Zody,M.
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------ Genome Center
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Lehoczky,J., Levine,R., Liu,G., MacLean,C., Macdonald,P.,
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Insert size: 202987; sum-of-contigs
Quality coverage: 10.8 in Q20 bases;
Quality coverage: 10.6 in Q20 bases;
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Center project name: L11075
Center clone name: 750_H_9
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3157: cor
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1216: contig of 2766 bp in
12716: gap of 100 hm
21088: contig of 8372 bp in length
21188: gap of 100 bp
27401: contig of 6213 bp in length
27501: gap of 100 bp
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35375: contig of 7874 bp in length
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3/30: contig of 2775 bp
50: gap of 100 hm
12616: con+:-
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i: contig of 2115 bp
p of 100
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                                                                                                                                                                                                            Local Similarity
                         APUUZ957 87834 bp. DNA PRI 26-APR-2001
Homo sapiens genomic DNA, chromosome 11q, clone:CTD-233717,
complete sequences AP002957
                                                                                                                                                                                                                                                                                             52691
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48290 c 49218 g
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138081. .158403
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27502. .35375
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4761. .6875
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158504. .194539
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12717. .21088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 87834)
Hattori,M., Ishii,K., Toyoda,A.,
Fujiyama,A., Yada,T., Totoki,Y.,
Direct Submission
                                                                           Submitted (08-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Nov 8, 2000 this sequence version replaced gi:7704958.
Draft Sequence Produced by DOE Joint Genome Institute
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www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence:
Estimated Total Number of Errors is 0.3.
                                                                                                                                                                                Direct Submission
Submitted (12-JAN-2000) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
3 (bases 1 to 151088)
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AC020917.4
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                                                 Finishing Completed at Stanford Human Genome Center
                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC020917
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Homo sapiens genomic DNA
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                                                                    www.jgi.doe.gov
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Location/Qualifiers
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Joint Genome Institute
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/db_xref="taxon:9606"
/chromosome="11"
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Primates;
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                                                                                                                                                                                               Facility,
Creek, CA
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and Sakaki, Y.
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Baker J., Baldwin J., Barna N., Beckerly R., Benn J., Brown A., Castle A.,
Cerny J., Colangelo M., Collins S., Collymore A., Cooke P., DeArellano K.,
Depayre E., Devon K., Dewar K., Donelan L., Doyle M., Ferreira P.,
PitzHugh W., Forrest C., Funke R., Gage D., Galagan J., Gardyna S.,
Gilbert D., Grant G., Hagos B., Heaford A., Horton L., Howland J.C.,
Jones C., Kann L., Karatas A., Lehoczky J., Lieu C., Locke K.,
Macdonald P., Marquis N., McEwan P., McGurk A., McKernan K., McLaughlin J.,
Miloff M., O'Connor T., O'Donnell P., Pavlin B., Peterson K., Pollara V.,
Riley R., Roberts D., Roy A., Severy P., Stange-Thomann N., Stojanovic N.,
Stone C., Subramanian A., Tesfaye S., Torruella-Miller I., Vassiliev H.,
Vo A., Wagner A., Wheeler J., Wu X., Wyman D., Ye W.J., Zody M.;
                                                                                                      Submitted Whitehead
                                     On Apr 1, 2000 this sequence version replaced gi:5332394 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 9 clone RP11-99J1 map 9, unordered pieces.
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05-APR-2000
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Center: Whitehead Institute/ MIT Center for Genome Research
           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Eutheria; Primates;
                                                                                          Cambridge,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Similarity 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHGC-57513 G37313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STS Content:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40571
                                                                                                     (02-JUL-1999) to the Institute/MIT Center
                                                                                          MA 02141,
                                                                                                                                                                                                                                                                                                                                                                                      Linton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                           chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CTD-2013N17"
38233 c 38536 g :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; HTG; 151366
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ome 9, clone
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pred. No.
                                                                                                      EMBL/GenBank/DDBJ databases for Genome Research, 320 Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Lander E.; RP11-99J1";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33748
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6.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                       Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                       Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
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Quality Coverage:.

* NOTE: This is a 'working draft' sequence. It currently 'consists of 9 contigs. The true order of the pieces 'is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.80774032459426Chemistry: Dye-primer amersham; Chemistry: Dye-terminator Big Dye; 4% of reads Assembly program: phrap; version 0.960731 Consensus quality: 136641 bases at least 040 Consensus quality: 145968 bases at least 030 Consensus quality: 148942 bases at least 020 Insert size: 158000; agarose-fp Insert size: 150566; sum-of-contigs
  Sequence 151366
                                                            misc_feature
                                                                                                                                   misc_feature
                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                      source
                                     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815; 96% of reads Sequencing vector: Plasmid; n/a; %-0.f%% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L8;
Center clone name: 99_J_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18666
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10529
18566
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4970 10
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/ 151366:
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18665: gap of 100 bp

26259: contig of 7594 bp 1

26359: gap of 100 bp

41183: contig of 14824 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                           81828:
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                                                                                                                                                                                                                                                                                                                                                                                           114786: contig of 32958 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18565: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4869: contig of 4869 bp in length
9: gap of 100 bp
10428: contig of 5459 bp in length
28: gap of 100 bp
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                                                         /note="assembly_fragment"
81829 114786
                                                                                                          /note="assembly_fragment"
41284 ...53957
BP; 46140 A;
                                                                                                                                                                                                            4970.
                                   /note="assembly_fragment"
114887. .151366
                                                                                                                                                                                     10529
                                                                                              /note="assembly_fragment"
                                                                                                                                    26360.
                                                                                                                                                             18666.
                                                                                                                                                                    /note="assembly_fragment"
                                                                                                                                                                                                                                              /clone="RP11-99J1"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                       /map="9"
                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                      /note="assembly_fragment"
                                                                                                                                            /note="assembly_fragment-clone_end:SP6~vector_side:right"
                                                                                                                                                                                              note-"assembly_fragment"
                                                                                                                                                                                                                     /note="assembly_fragment~clone_end:T7~vector_side:left"
                                                                                                                                                                                                                                                                                                          /chromosome="9"
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28257 G;
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800 other;
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COMMENT
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AC011980/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced gi:0453966.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Baldwin, J., Barna, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooke, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-16H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC011980.3 GI:7230122
HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown, A., Castle, A., Colangelo, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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NOTE: This is a 'working draft' sequence. It currentle consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 153733)
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(bases 1 to 153733)
                                                                                                                                                                                                              Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 117952 bases at least Q40
Consensus quality: 136478 bases at least Q30
Consensus quality: 146705 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 4.1 in Q20 bases; Quality coverage: 4.2 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                             Insert size: 157000; agarose-fp
Insert size: 152733; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L3543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Castle, A., Colangelo, M., Collins, S., Collymore, A., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                           100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                           agarose-fp
sum-of-contigs
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                                                            It currently
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 23
AL592213/c
                                                                                              Db 120518 AAAAACAAAACACAAACATAAAG
                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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                                                                                                                                                                                           Query Match
Best Local :
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                                                                                                                                 1152 aaaaacaaacacaaacataaag 1173
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76307 89151: contig of 12845 bp in
89152 89251: gap of 100 bp
89252 107693: contig of 18442 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment" 24294. .37092
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9513. .14144
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/db_xref="taxon:9606"
/clone="RP11-16H7"
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107794. .153733
/note="assembly_fragment"
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 155531 bp
                                                                                                                                     0.7%; Suc.
100.0%; Pred. No.
100.0%; Mismatches
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22; Conserv
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On Aug 9, 2001 this seguence version replaced of iterators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 30% of reads
Sequencing vector: plasmid; L08752; 69% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads Chemistry:
 AP002958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 155531; sum-of-contigs
Insert size: 144681; 16.2% error; agarose-fp
Quality coverage: 15.49x in Q20 bases; sum-of-contigs Quality
coverage: 16.65x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 155436 bases at least Q40 Consensus quality: 155453 bases at least Q30 Consensus quality: 155482 bases at least Q20
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Chemistry: Dye-primer-amersham; 28% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Sanger |
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www-seq.wi.mit.edu
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Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Aug 9, 2001 this sequence version replaced gi:15029558. Draft Sequence Produced by Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:
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/db_xref="taxon:9606"
/chromosome="9"
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114991 125640 contig of 10650 bp in length
114991 125640 contig of 8730 bp in length
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134571 140147 contig of 5577 bp in length
140248 147375 contig of 7128 bp in length
147476 150473 contig of 2998 bp in length
150574 153025 contig of 2452 bp in length
153126 155065 contig of 1940 bp in length
153126 156230 contig of 1940 bp in length
153126 156230 contig of 1065 bp in length
15516 156230 contig of 1065 bp in length
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Submitted (28 NOV-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
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AP002958
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                                                                                                                                                                                            is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                              as soon as it is available and the accession number will be preserved.
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Quality coverage: 8.02x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: RP11-16H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: HumDraft11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://hgp.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: RIKEN Genomic Sciences Center(GSC)
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     32099: contig of 32099 bp
99: gap of 100 bp
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14063 bp
1378 bp
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14063 bp
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Q

Query Match Best Local Matches 2

22; Conser

0.7%; 100.0%;

Score 22; Pred. No.

DB 2;

Length 156230;

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Mismatches

Indels

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Gaps

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BASE COUNT
ORIGIN
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155066 155165: gap of 10
155166 156230: contig of 1
1500atton/Qualifiers
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150474 150573:
150574 153025
153026 153125:
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147476 150473: contig of
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134571 140147: contig of 5577
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62729 62828:
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46805 46904:
                                                /note="assembly_fragment"
155166. .156230
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                                                                                                                                                                                                                                                                                                                                          90484
                                                                                                                                                                            /note="assembly_fragment"
140248. .147375
                                                                                                                                                                                                          /note="assembly_fragment"
134571. 1401/7
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100662 ..114890
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/db_xref="taxon:9606"
                                                                                                                                              L47476. .15047
                                                                                                                                                          note="assembly_fragment"
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76992. .90383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on Nov 22, 2000 this sequence version replaced gi:9886030. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-AUG-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L.,
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                        NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 159946)
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                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; n/a; 100% of read Sequencing vector: Plasmid; n/a; 100% of read Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 consensus quality: 139893 bases at least 030 consensus quality: 150490 bases at least 030 consensus quality: 154263 bases at least 020
                                                                                                                                                                                            Insert size: 176000; agarose-fp
Insert size: 156346; sum-of-contigs
Quality coverage: 3.2 in Q20 bases; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
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This record will be updated with the finished sequence as soon as it is available and the accession number wi
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5198 6297; gap of 29
8221; corrigor 22
8321; gap of 22
8221; corrigor 23
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2698 3739: co
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9658: gap of 100 bp
11181: contig of 1523 bp in length
11281: gap of 100 bp
                                                                                                                       130770:
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56439: contig of 2508 bp in
339: gap of 100 hn
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92085: contig of 4956 bp
185: gap of 100 bp
97647: contig of 566 bp
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contig of 9750 bp
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158960 159059: gap of 100 bp
159060 159946: contig of 887 bp in length.
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69918. .73103
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51237. .53831
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/db_xref="taxon:9606"
/chromosome="11"
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                                                                                          Query Match 0.7
Best Local Similarity 100
Matches 22; Conservative
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 7% of reads Chemistry:
Dye-terminator Big Dye; 92% of reads
Consensus quality: 185600 bases at least Q40
Consensus quality: 185966 bases at least Q30
consensus quality: 185182 bases at least Q20
Insert size: 186313; sum-of-contigs
Insert size: 140000; 37.9% error; agarose-fp
Quality coverage: 9.01x in Q20 bases; sum-of-contigs Quality
coverage: 12.46x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186413)
Mashreghi-Mohammadi,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 9 clone RP11-64P11, PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: bA64P11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
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168557 18641
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168557. .186413
/note="assembly_fragment:00456"
. 35149 c 33874 g 56599 t
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1. .168456
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-64P11"
                                                                                                                                                                                                                                                                                                                                                  note="assembly_fragment:00638
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18556: gap of 100 bp 
186413: contig of 17857 bp in length.
                                                                                       0.7%; Score 22; DB 100.0%; Pred. No. 6. tive 0; Mismatches
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6.2;
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BTCASK35
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                BTCASK35 7
Bovine gene fo x14908 x14326 x14908.1 GI:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 128, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 25, 2001 this sequence version replaced gi:14787678.
casein; kappa-casein; repetitive sequence: Alu-like repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coverage: 10.54x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: bA187G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Sanger Centre
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Mammalia; Eutheria; Primates;
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Homo sapiens chromosome 9 clone
PROGRESS ***, in ordered pieces.
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                   GI:180
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36707 c 36581 g 59596 t
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/clone_lib="RPCI-11.1"
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/chromosome="9"
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Mackinlay, A.G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-MAR-1989) A.G. Mackinlay, The University of New South Wales, P.O. Box 1 Kensington New South Wales Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapping, and polymorphism Mamm. Genome 5 (5), 288-297 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaiman,D., Mercier,D., Moazami-Goudarzi,K., Eggen,A., Vaiman,D., Lepingle,A., Velmala,R., Kaukinen,J., Varvio,S. Martin,P. et,al.
A set of 99 cattle microsatellites: characterization, synteny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolation and characterization of the bovine kappa-casein gene Eur. J. Biochem. 178 (2), 395-401 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 7595)
Alexander, L.J., Stew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence; restriction fragment linked polymorphism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=kc_mat
/product="kappa-casein"
4930. .5412
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2886. .2891
                                 /note="t is c
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to atc (Ile)"
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/db_xref="taxon:9913"
 /note="g is a
7570. .7571
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site, creates
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/usedin=X14907:kc_sig
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7296. .7416
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3 (bases 1 to 37906)
Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E., Ricke,D.O., Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S., Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J., Goodwin,L., Bryant,J., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M., Misra,M. and Deaven,L.
                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-JUN-1998) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 37906)
Ricke,D.O., Bruce,D., Mundt,M., Doggett,N., Munk,C., Saunders,E.,
Robinson,D., Jones,M., Buckingham,J., Chasteen,L., Thompson,S.,
Goodwin,L., Bryant,J., Tesmer,J., Meincke,L., Longmire,J.,
White,S., Ueng,S., Tatum,O., Campbell,C., Fawcett,J., Maltbie,M.,
Misra,M., and Deaven,L.
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/note="97% identity EST yb12f02.rl"
/db_xref="dbEST:T47043"
6373. .6501
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4130. .4301
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1 1292 c 1182 g 2475 t
               /rpt_family="L1" 7898. .10788
                                                                                                         /rpt_family="MER25" 6572. .6858
                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="330D11"
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7509. .7828
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7074. .7299
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                 fruit fly
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complement(31921. .32340)
/rpt_family="MLTI"
33481. .33615
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/rpt_family="MLT1d"
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complement(30385..30580)
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18375
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33613. .34213
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note="GRAIL 2 excellent exon, frame 0"
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/rpt_family="L1"
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/rpt_family="MIR2"
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/rpt_family="MER21"
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14119. .14293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family-"L1"
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                                                             JOURNAL
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                                                                                                                                         Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Hawland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., Naylor, J., Minova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T., Norman, C., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thodore, J., Tirrell, A., Travers, M., Tilgilio, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Tilgilio, J., Ve, W.J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Submitted (26-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10212758 by the submitter For more information on this record e-mail to fly@celera.com.
                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 3, clone RP11-334K8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 45496)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                 Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or more information on this record e-mail to fly@celera.or
NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
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Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This record contains 86 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
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                                                                                                                                                                                                                                                                                                             8767 8866: gap of 100 bpr
8867 9669: contig of 803 bp
9670 9769: gap of 100 bp
9770 10559: contig of 790 bp
10560 10659: gap of 100 bp
11450 11549: gap of 100 bp
11450 11549: gap of 100 bp
11450 12330: contig of 781 bp
12331 12430: gap of 100 bp
12431 1322: contig of 792 bp
13223 13322: gap of 100 bp
1323 1322: gap of 100 bp
1323 1322: gap of 100 bp
1323 13409: contig of 792 bp
1323 13409: contig of 792 bp
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----- Project Information
Center project name: L7376
Center clone name: 334_K_8
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17656 17755:
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14199 14992: contig of 794 bp in length
14993 15092: gap of 100 bp
15093 15881: contig of 789 bp in length
15882 15981: gap of 100 bp
15882 16771: contig of 790 bp in length
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904 1690: cc
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20 6219: gap of 100

10 6998: contin - 7

9 7000.
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8766: contig of 782 bp in
8866: gap of 100 hr
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5998: contig of 779 bp in

7098: gap of 100 bp

7884: contin - 7
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18649: gap of 100 bp
19440: contig of 791 bp
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40: gap of 
23041: contig
               36: gap of 100 k
22140: contig of 804
40: gap of 100 k
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                                                                            50659: contig of 804 bp i

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51542: contig of 783 bp i

3 51642: gap of 100 bp

3 52427: contig of 785 bp i

8 52527: gap of 100 bp

18 52527: gap of 801 bp i
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44448: cor
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82 37276: contig of 795 bp in 16
77 37376: gap of 100 bp in 16
77 38182: contig of 806 bp in 16
83 38282: gap of 100 bp in 16
83 38282: contig of 790 bp in 16
84 30172: contig of 790 bp in 16
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J: contig of 775
J: gap of 100 b
48863: contig of 780 bp
48963: gap of 100 h
48965: contig of 780 bp
7855: contig of 7855; gap of
                                              53428: gap
54211:
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46220: conf
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33831: gap of 100 bp
34582: contig of 751 bp in 1
34682: gap of 100 bp
35480: contig of 798 bp in 1
15580: gap of 100 bp
36381: contig of 801 t-
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48 59647: gap of 100 bp
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4777 sara
                                                            /note="strong similarity to actin depolymerizing factor1, Arabidopsis thaliana, PATCHX:G1408471 Contains Actin depolymerizing proteins signature,
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Contains Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature & profile, [YKGTPFHRIISGFVIQGG]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHRIISGFVIQGGDIIHGDGKSSDSIYGGTFPDENFKIQHSHAGMVAMANTGPDSNGS
QFFITTVKASWLEGEHVVLGKVIQGMDNVFAIEGGAGTYSGKPRKKVVIADSGEIPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="cyclophilin-like protein"
/protein_id="CAA17761.1"
/db_xref="GI:2924507"
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/gene="M4E13.30"
Join(9714. 9955,10256. .10406)
/gene="M4E13.30"
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5954. .6029,6297. .6459)
/gene="M4E13.20"
/product="actin depolymerizing factor-like protein"
/protein_id="CAA17762.1"
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complement(12742.
/gene="M4E13.40"
 complement(17840.
                               complement(17745.
                                                                                                                              /product="MYB-like protein"
/protein_id="CAA17764.1"
/db_xref="GI:2924510"
/db_xref="SPTREMBL:049608"
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GLQRCGKSCRLRWINYLRPDLKRGNFTLEEDDLIIKLHSLLGNKWSLIATRLPGRTDN
EIKNYWHYNKKLLRKGIDPATHRPINETKTSQDSSDSSKTEDVKILSFGPOLEK
IANFGDERLGKRVEXSYVEERCLLMLELRISPPWQDKLHDERNLRFGRYKYRCSSCR
FGFGNGKECSCNNYKCQTEDSSSSSYSSTDISSSIGYDFLGLNNTRVLDFSTLEMK"
                                                                                                                                                                                                                                                                                                                                                                                                                                      family signatures, [LPRSAGLORCGKSCRL],
site motif A (P-loop), [GLORCGKS]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="strong similarity to myb-related protein Y49, Arabidopsis thaliana, PIRI:S5829 Contains myb DNA-binding domain repeat signatures, [WTKEEDDKI][WSLIATRIPGRTDNEIKNYWNTHY], Aldo/keto reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(17183. .17744,17840. .18102))
/gene="M4E13.50"
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GGGDGITSPYYLDPIAIGSYGAASKGIFVSSSAGNEGFNGMSVTNLAPWTTVCASTI
DRWFPADAILDGHRLRGVSLYAGVPLNGRWFPVVPFKSGMSSASLCMENTLDPXQV
RGKIVICDRGSSPRVAKGLVVKKAGGVGMILANGASNGEGLVGDAHLIPACAVGSNEG
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SPQFLGLQNQKGLWSESDYGSDVIIGVFDTGIWPERRSFSDLNLGPIPKRWRGVCESG
ARFSPRNCNRKIIGARFFAKGQQAAVIGGINKTVEFLSPRDADGHGTHTSSTAAGRHA
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Arabidopsis thaliana, PIR2:S52770
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/translation="MTDDCKKSSMEMKWKKVHRYVVYKLEEKSRKVTVDKVGAAGESY
DDLAASLPEDDCRYAAVEPDYVTVDWCRMSKIFFITWSPEASRIREKMMYATSKSGLR
RVLDGVHYELQATDPTEMGFDKIQDRAK"
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MMTTTNLVDNSNRSLIDESTGKSATPYDYGSGHLNLGRAMNPGLVYDITNDDYITFLC
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/protein_id="CAA17763.1"
/db_xref="GI:2924509"
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                                                                                                                                                                              translation="MGRSPCCEKDHTNKGAWTKEEDDKLISYIKAHGEGCWRSLPRSA"
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REFERENCE
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AUTHORS
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ATT12J5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (22-FEB-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de.mayer@mips.biochem.mpg.de.project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              project).
AL035522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome viewed at: http://websvr.mips.blochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory, John Innes Centre, Colney Lane, NR4 E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 84499)
EU Arabidopsis sequencing, project.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bevan, M., Murphy, G., Ridley, P., Hudson, S., Hoheisel, J., Mewes, H.W., Mayer, K.F.X. and Schueller, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Ensicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                             /gene="T12J5.10"
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/gene="T12J5.10"
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NNVFQAKFMPFSDDRTIVTCAADGMFDLRTEAPTELFTCRSVDPRRRNMDAIQLNAIA
                                                                                                                                                                                                                                                                    refer to this entry"
48992. .51335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(20820. 21014,21397 .21499,21644.
21807 .21889,22003. 22051,22140. 22205,22752. ..
22966. .23090,23242. .23354))
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complement(join(20820. .21014,21397. .21499,21644.
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O-methyltransferase, Pinus taeda, gb:U39
                                                                                                                                                                                                                            complement(join(55847. .56170,56842.
/gene="T12J5.30"
                                                                                                                                                                                                                                                                       complement(join(55847./gene="T12J5.30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(52611.
/gene="T12J5.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMMITKLHGKDLWAFAQDNLCHSQLINEAMACDARRVVPRVAGACQGLFDGVATVVDV
GGGTGETMGILVKEFPWIKGFNFDLPHVIEVAQVLDGVENVEGDMFDSIPASDAVIIK
WVLHDWGDKDCIKILKNCKEAVLPNIGKVLIVECVIGEKKNTMIAEERDDKLEHVRLQ
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O-methyltransferase, Pinus taeda, gb:U39
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/gene-"T1205.20"

complement()oin(51806. .52129,52611.

/gene-"T1205.20"
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/gene="T12J5.20"
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FSEQSELLVSYNDEFYYLFTPOMGLGSNPIPSSPISSPKSENSSSSPKDENEESVS
LVYKGHKNCETVKGVNFFFPRSEYVVGGSDCGRIFIRKKGGELIRVMEADRHVVNCI
EPHPHLPVLASSGIESDIKVWTSKAAERATLFENIELLPSRFRIPMLSFLSFHDYDDE
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                                                                                                                                                         contains EST gb:N96576,
                                                                                                                                                                                                                                                                                                                                                  55847
                                                                                                                                                                                                                                                                                                                                                                                        complement(53065.
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/gene="T12J5.10"
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DGLATGYVNTPLSRRLMITRRDGKSLAPFVLFETTPEMLA&WLRLSSVVSSPVNGSTP
                                                                                                                                                                                                                                                                                                                       /gene="T12J5.30"
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                                                                                                                                                         Pinus taeda,
76, W43582"
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PPFDAVHGKDVWSFAQDNPFLSDMINEAMACDARRVVPRVAGACHGLFDGVTTMVDVG

VLHDWGDKDCIKILKNCKEAVPPNIGKVLIVESVIGENKKTMIVDERDEKLEHVRLML

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/gene="T1205.50"
/note="strong similarity to Lily mRNA, Lilium longiflorum,/note="strong similarity to Lily mRNA.
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/protein_id="CAB36724.1"
/brotein_id="CAB36724.1"
/db_xref="GI:445343"
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NDQGQVSNFQHHSVAESSSYPRSSGPLRNEYSSVQVHDLDRRTHEDEDYDEMDGPDEK
RRRITRFYSCLLFTLVLAFTLFCLILMGVSKSFAPIATLKVIDRFDRLERENFTFISV
                                                                                                                                                                                                                                                                                                                                    AACFIHLTFIFSCLCSYPINLMPACDNIEMVYITKKKKPASIIVRMMLRVFLSLVCFTIAVGFPFLPYLAVLIGAIALLVTFTYPCFMWISIKKPQRKSPMWLFNVLVGCLGASLSVLLLVASAMRLAQKGLHANFFRP
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                             complement(64870.
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/gene="T12J5.50"
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/gene="T12J5.50"
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                                                                                                                         complement(64552.
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AL022604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-APR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de.mayer@mips.biochem.mpg.de roject Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes and 5 can be viewed at: http://www.mips.biochem.mpg.de/pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 86710)
EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E-mail: michael.bevan@bbsrc.ac.uk
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/VESIGLGSEPAFKVDDYDFRSPGELPLYLLLGALCGLVSLALSRCTSSMTSAUDSLNK
VSEIGLGSEPAFKVDDYDFRSPGELPLYLLLGALCGLVSLALSRCTSSMTSAUDSLNK
DAGIFRAVFPVMGGLSVGITALVYPPULYMGFQNVDILLEKAPVGLSADLLLQIVA
VKIAATAWCRASGLVGGYAPSLFIGGAAGMAYGKFIGLALQUPDFNLSILEVASPQ
AYGLVGMAATLAGVCQVPLTAVLLLFELTQDYRIVLPLLGAVGNSSWITSGQSKRQET
RETKETRKKKQQEAYQSLTSSDDESSTNNLCEVESSLCLDDSLNQSEELPKSIFVSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="F23E12.10"
173. .374
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173. .1890
                                                                                                           HPVGVLDRECITLTRR"
                                                                                                                                                                                                                                                                             /product="hypothetical prot
/protein_id="CAA18726.1"
/db_xref="GI:3080407"
/db_xref="SPTREMBL:065486"
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/codon_start=1
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/variety="Columbia"
/db_xref="taxon:3702"
                                                                                                                               NRPKDIFVNDICSRSGGKCKVPWTVTPDMDLLAAQTIMNKHELSHVAVVSGSIDAPRI
                                                                                                                                                  /gene="F23E12.10"
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Pred. No.
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/gene="F23E12.30"

complement()oin(4939. .5013,5109. .5195,5307. .5342,

5451. .5651,5725. .5811,6161. .6163))

/gene="F23E12.30"

/note="Contains Clathrin adaptor complexes small chain signature [VVYKRYASLYF]

contains EST gb:T44219"
                                                                                                                                                                                           complement(join(4939.
5451..5651,5725..58
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4939..6163
                                /product="clathrin assembly
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                                                                                                                                                                                                                                                   /gene="F23E12.20"
/number=5
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/number=4
4211. .4428
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SCRKNPSLKRVVLTSSSSTVMYALSKTLAEQAAWKFSBENGIDLVTVLPSFLVGPSLP
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x sp., PIR2:S35189"
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4211. .4428)
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.5811,6161. .6163))
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/gene="F23E12.40"

complement(7352. .7582)

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complement(8233. .9045)
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Direct Submission
Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Submitted (21-AUG-1999) Genome Sequencing Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington Center, Washington C
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Waterston, R.H.

Direct Submission
Submitted (28-AUG-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (12-JUN-1998) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Waterston,R.H.
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                          63108,
Feb 3,
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22237 c 22107 g
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , 1999 this sequence version replaced gi:3213090 Location/Qualifiers
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                        2001 this sequence version replaced gi:11415227
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Center code: WIGSC
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Insert size: 156208; sum-of-contigs
Quality coverage: 5.45 in Q20 bases; agarose-fp
Quality coverage: 5.28 in Q20 bases; sum-of-contigs
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Consensus quality: 151471 bases at least Q40
Consensus quality: 153455 bases at least Q30
Consensus quality: 154315 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-primer ET; 93% of reads Chemistry: Dye-terminator Big Dye; 6%
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------ Project Information -------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence {\sf T}
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1. .157308
                        /note="assembly_name:Contig15"
71747. .96546
                                                                  vector_side:left"
53684. .71646
                                                                                                                                                                                                             /note="assembly_name:Contig12"
27493. .38821
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16405. .27392
                                                                                                                clone_end:T7
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/db_xref="taxon:9606"
/chromosome="7"
/note="assembly_name:Contig16"
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ig of 24800 bp in
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                                                                                                                                                    Consensus quality: 172462 bases at least Q40 consensus quality: 17746 bases at least Q30 consensus quality: 178816 bases at least Q20 Estimated insert size: 163610; agarose-fp estimation Estimated insert size: 182539; sum-of-contigs estimation Quality coverage: 14.49 in Q20 bases; agarose-fp estimation Quality coverage: 12.99 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
                                     * consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US On Apr 25, 2001 this sequence version replaced gi:9954669.
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Homo sapiens chromosome 16 clone RP11-487C14,
SEQUENCE, 14 unordered pieces.
                                                                                                                                                                                                                                                                                                                                Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                  Center clone name: RPCI-11_487C14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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DOE Joint Genome Institute.
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150421. .153662
/note="assembly_name:Contig8"
153763. .157308
/note="assembly_name:Contig9
clone_end:SP6
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/note="massembly_name:Contig17"
119735. .146540
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REFERENCE
AUTHORS
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SOURCE
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AC013553/c
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                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
         McEwan, P.,
                          Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-325L12
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 184864)
                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                   AC013553 184864 bp DNA HTG 13-DEC-2000 HOMO Sapiens chromosome 15 clone RP11-325L12 map 15, *** SEQUENCING IN PROGRESS ***, 1 ordered pieces.
                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                      AC013553
                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                         AC013553.14 GI:11693406
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5575
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6833
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/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-487C14"
/clone_lib="RPCI human BAC library 11"
37425 c 39803 g 55084 t 1308 others
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McGurk, A., McKernan, K., Naylor, J., Norman, C.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29505: gap of unknown length 38983: contig of 9478 bp in 1 39083: gap of unknown length 69212: contig of 30129 bp in 69312: gap of unknown length
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10923:
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              Meldrim, J.,
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COMMENT

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              Direct Submission
Submitted (23-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Dec 13, 2000 this sequence version replaced gi:9280765.
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                     HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                              Waterston, R.H.
                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                              Homo sapiens chromosome
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                                                                                           Unpublished
                                                                                                           The sequence of Homo sapiens clone
                                                                                                                            Waterston, R.H.
                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                     AC080090.3 GI:11345029
                                                                                                                                                                                                                                                              29 unordered pieces.
                                                                                                                                                                                                                                                                                                AC080090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of I contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
1 184864: contig of 184864 bp in length.
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                                                                            (bases 1 to 194874)
                                                                                                                                           (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                   HTGS_PHASE1; HTGS_DRAFT
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    USA
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/clone_lib="RPCI-11 Human Male BAC"
42968 c 41143 g 49479 t
                                                                                                                                      ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 to 194874)
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                   Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 3.95 in Q20 bases; agarose-fp Quality coverage: 4.25 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 202000; agarose-fp
Insert size: 191473; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
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                       'note="assembly_name:Contig38"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV81 at the 5' end and an overlap with ATCHRIV83 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-ma Elemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambri Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, John Laboratory, Laboratory, John Laboratory, John Laboratory, John Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, Laboratory, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-mail: michael.bevan@bbsrc.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicota; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 29459 to 132608; 129923 to 195155)
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LAGLSAGMAIGIVGDAGVRANAQQPKLFVGMILILIFAEALALYGLIVGIILSSRAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Contains Prokaryotic membrane lipoprotein lipid attachment site AA16-26; Prokaryotic membrane lipoprotein lipid attachment site AA91-101 contains EST gb:741774, N95995, N38619, Z26112, N38618, AI998496.1, AI996086.1, R90087, AA712128, H76763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="AT4g34720"
complement(23001.
/gene="AT4g34720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQLKQRCVEGFKEGVLSIEQLASVDGLCEWVLKAIGASDPVHTYNINLSVFTSIPDLW
GIDQLFPIVPIHKLDQRPGARGILSDLTCDSDGKINKFIGGESSLPLHELDKNGSGGR
YFLGMFLGGAYEEALGGVHNLFGGPSVVRVSQSDGPHSFAVTRAVPGQSSADVLRAMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLSSSLYRIDGWGAPYFIANSGNISVRPHGSETLPHQDIDLLKIVKKVTGPKSSGL
GLQLPLLVRFPDVLKNRLECLGSAFDYAIKSQGYDSHYGVGVDYWGDUYK
FGSSFREGLBAGSKPEILLAMSGLCKGSPDBFLYCNGFKDAEYISLALLGRKLALTUY
IVLEQEEELDLVIELSQKMNVRPVIGLRAKLRTKHSGHFGSTSGEKGKFGLTTTQIVR
VVRKLROSGMLDCLQLLHFHIGSQIPSTSLLSDGVAEAAQLYCELVRLGAHMKVIDIG
GGLGIDYDGSKGGESDLSVAYSLEFAYAEVVASAYRVVCDRSSVKHPVLGSESGRAIVS
HHSVLIFEAVSADKPMVHQATPGDIQFLLEGNEEARANYEDLYAAVMRGDHESCLLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Contains Orn/DAP/Arg decarboxylases family signatures AA144-162;Orn/DAP/Arg decarboxylases fasignatures AA325-338
                                                                                    /note="similarity to similarity predicted protein, Synechocystis sp., PIR2:876285 contains EST gb:F19817" /codon_start=1
                                                                                                                                                                                                                                                             24797. .25047

/gene="AT4g34730"

/gene=tc/join(24797. .24955,25226. .25399,25678.

/gene="AT4g34730"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASPSNSLSAAISNLGFYYCDEDVYDYISA" complement(15093. .17228)
                                                                                                                                                                                                      complement(join(24797. .24955,25226. .25399,25678.
/gene="AT4g34730"
                                                                                                                                                                                                                                                                                                                                                                                                       complement(23868.
/gene="AT4934720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(23231.
/gene="AT4g34720"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="AT4g34720"
complement(join(23001. .23133,23231. .23516,23868. .23943))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AT4g34710"
complement(join(23001. .23133,23231. .23516,23868. .23943))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contains EST gb:W43783,
AI998693.1, AA404845"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(23517.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="arginine_decarboxylase_SPE2"
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/product="putative protein"
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/db_xref="GI:7270424"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AT4g34720"
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                                                                                                                                                                                                                                                                                                                                                                                  /number=3
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Query Match 0.7%;
Best Local Similarity 100.0%;
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On Aug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibbs, R.
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Mammalia; Eutheria;
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    NOTE: Estimated insert size
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 195217)
                                                                              Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 17% of reads
Chemistry: Dye-terminator Big Dye: 83% of reads
Assembly program: Phrap; version 0, 990329
Consensus quality: 151852 bases at least Q40
Consensus quality: 155851 bases at least Q30
Consensus quality: 174484 bases at least Q30
Consensus quality: 175615; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; squarose-fp estimation
Quality coverage: 3.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: HAJY Center clone name: RP11-50102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
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Pred. No.
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3 clone RP11-50102, WORKING DRAFT SEQUENCE,
may differ from sequence length
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. 21;
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REFERENCE

AUTHORS

SOURCE

ORGANISM

KEYWORDS CESSION AC025566/c RESULT 41

Matches.

Locus

EFINITION

COMMENT

JOURNAL FERENCE AUTHORS

JOURNAL

TITLE

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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NOTE: This is a 'working draft' sequence. It currently
consists of 40 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved
                                                                                                  166904
169179
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153032
157665
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                            Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                          4 (bases 1 to 24256)
Murphy,G., Ridley,P.,
Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 16641 to 103350)
                                                                                                                     Direct Submission
                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                  Rose, M., Hempel, S.,
Mayer, K.F.X.
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                                                                                                                                                                                                                                                                                                       Robben, J., Grymonprez, B.,
                                                                                                                                                                                                                                                                                                                                  Unpublished
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/db_xref="taxon:9606"
/chromosome="3"
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Location/Qualifiers
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12314. .12457 17464
/translation="MAVSFHVRSNSYPSRQHPQAAHVDEQLTRLRSSDSASSSSICQR
LSNLQDLHDSLEKMIRLSVTNLALSQDQIEKLLDGSLRILDLCNIAKDAISQMKEGLM
EIQSILRRKPGDLSGEVKKYLVSRKFLKKSLQKVIKSLKVCQSKDSTNASLVVFGRAE
                                                                                                                                                                          /gene="AT4g35200"
complement(13757.
                                                                                                  Arabidopsis thaliana"
                                                                                                                                             /gene="AT4g35200"
complement(13757.
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ESLENLKWVTRRLNLVYGGGSIGLMGLVSQAVHEAGGHVLGYAAIYDLFTLTGETYG
EVIAVADMHERKAEMARHSDCFIALÞGGYGTLEELLEVIAMAQLGIHDKPVGLLNVD
YVNYLLTFIDKAVDDGFIKÞSQRHIFVSAÞNAKELVQKLEILMKINKDKKFDSAIDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity to ctf, Mycobacterium leprae, gb:U15180
contains EST gb:T45691, T22640, T75954"
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/note="similarity to various
                                                                                                                                                                                                       13757. .14518
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/variety="Columbia"
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17252. .]
                                                                 thaliana, PIR2:S28615 contains EST gb:AI997799.1, F13911"
                                                                                                                                complement join (19941...20231, 20345...20792...20980, 21340...21425, 21551....20798...22213, 22304...22657))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="position 76883-84499 overlaps to BAC clone F23E12 EMBL acc:AL022604; for sequence analysis please refer to this accession"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative protein"
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IALFESLFSFMSGSKACGKWSLVSKMMSQSKGTCEAEANEFTRVDMEFQSEKSLQMED
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Arabidopsis thaliana"
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join(17252. 17657,17740. 17784,18534.
/gene="AT4g35220"
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16043. .16795
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ACCESSION
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AUTHORS
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                     On Jan 19, 2001 this sequence version replaced gi:10280764. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996–1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
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Homo sapiens chromosome 15 cla
SEQUENCE, 12 unordered pieces
                                                                                                               Submitted (04-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boguslavkiy,L.,
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LFHWENQTIEWAMRLRVGYYIAEALDYCSTEGRPLYHDLNAYRVLFDEDGDPRLSCFG
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IRGKNIILLMOSHLEGKFSTEBATVVVELBASQCLQYEBRERPWINDAYLAPLQTKS
DVPSSYVMLGKKQEEAPSTPQRPLSPLGEAGSRMDLTAIHQILVMTHYBDDEGTNLSE
SVENGYMGKKQEEAPSTPQRPLSPLGEAGSRMDLTAIHQILVMTHYBDDEGTNUSS
FQEWTQQMKDMLDARKRGDQSFREKDFKTAIDCYSQNSYGYIHCFCGQFIDVGTMYSP
TVFGRRSLCYLLCDQDDAALRDAMQAQCVYPDWPTAFYMQSVALAKLNMNTDAADMLN
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Pred. No.
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clone RP11-540E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
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5, WORKING DRAFT
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Insert size: 197835; sum-of-contigs
Quality coverage: 10.6 in Q20 bases; agarose-fp
Quality coverage: 8.9 in Q20.
NOTE: This is a 'working draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
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be preserved.
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4883 4982: gap of 100 bp
5624: contig of 642 bp in length
5625 5724: gap of 100 bp
5725 6734: contig of 1010 bp in length
6735 6834: gap of 100 bp
6835 8393: contig of 1559 bp in length
8394 8493: gap of 100 bp
11417 11316: contig of 2823 bp in length
11317 11416: gap of 100 bp
11417 16171: contig of 4755 bp in length
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Consensus quality: 19333 bases at least Q40 Consensus quality: 195810 bases at least Q30 Consensus quality: 19588 bases at least Q20 Consensus quality: 19588 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L10276
Center clone name: 540_E_6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     soon as it is available and the accession number will
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/db_xref="taxon:9606"
/chromosome="15"
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                                                                                                                                         /note="assembly_fragment"
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|6272. .30341
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180063: contig of 21541 bp in
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AL593857/c
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                                                                                                                                                                                                                                                                                                                 Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LO8752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 204045 bases at least Q40
Consensus quality: 204532 bases at least Q20
Consensus quality: 204577 bases at least Q20
Insert size: 205337; sum-of-contigs
Insert size: 205337; sum-of-contigs
Ouality coverage: 10.60x in Q20 bases; sum-of-contigs Quality coverage: 10.47x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bM439H2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Sanger Centre
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                           /db_xref="taxon:10090"
/chromosome="2"
                                                                                     /organism="Mus musculus"
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L513468/c
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Best Local Similarity
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                                                                                                           Submitted (20-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 27, 2001 this sequence version replaced gi:13568261.
                           Center project name: bM10416
                                                  Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
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AL513468.5 GI:13872411
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus chromosome X clone RP23-10416, PROGRESS ***, in unordered pieces.
                                                                               Web site:
                                                                                                 Center code: UK-MRC
                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                     Tromans, A.
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 211030)
                                                                                                                                                                                                                                                                                                                     house mouse.
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/note="assembly_fragment:05216
fragment_chain:1"
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46386. .1
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fragment_chain:1"
150562. .161265
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47684 c 46179 g
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fragment_chain:1"
146349. .150461
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fragment_chain:2
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fragment_chain:2"
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1. .15760
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fragment_chain:1"
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fragment_chain:1"
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                                                                            http://mrcseq.har.mrc.ac.uk
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Summary Statistics am: XGAP4; version
                                              Project Information
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Pred. No.
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AC092992/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 221341)

CE 1 (bases 1 to 221341)

Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Alsbrooks, S. L., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S. L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowite, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Benton, J., Charvez, D., Chen, C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Dayis, C., Day-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwalte, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisl, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Gabisl, A., Gao, J., Garcia, A., Garner, T., Farntz, P., Gabisl, A., Gao, J., Garcia, A., Garner, T., Garza, N., Garres, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Johoson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Levis, L.C., Liu, W., Lekls, L., Liu, W., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, 20 unordered pieces. AC092992
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* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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/chromosome="X"
/clone="RP23-10416"
/clone_lib="RPCI-23"
1. .166819
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40504 c 38146 g 61675 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (09-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 20 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 212184 bases at least Q40
Consensus quality: 217356 bases at least Q30
Consensus quality: 220392 bases at least Q20
Estimated insert size: 220263; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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AUTHORS
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         MO 63108, U
On Sep 10,
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Submitted (08-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                    Center: Washington
Center code: WUGSC
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 227194) Waterston, R. H.
Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                       Waterston, R.H.
                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                             The sequence of Homo sapiens clone
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38966 c 37158 g
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/db_xref="taxon:9606"
/chromosome="3q"
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200992: gap of unknown I

205927: contig of 4935 b

206027: gap of unknown I

210855: contig of 4828 b

210955: gap of unknown I

214834: contig of 3879 b

214934: gap of unknown I

214936: contig of 2942 b

217976: gap of unknown I

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Insert size: 226623; sum-of-contigs
Quality coverage: 4.11 in Q20 bases; agarose-fp
Quality coverage: 4.19 in Q20 bases; sum-of-cont
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/chromosome="3"
    /note="assembly_name:Contig10"
|0599. .13494
                                                                                                /note="assembly_name:Contig8"
                                                                                                                                                                                 /note=
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of 1062
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            Pablos, B.,
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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133033, .154508
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185859. .227194
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154609. .185758
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37424. .47954
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13595. .17577
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                                                                                                                                                                                                                                                                                                                                                                      melanogaster
Doup, L.E.,
                  Delcher, A.,
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                    Deng, Z., Mays, A.D.,
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21;
Dugan-Rocha, S.,
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Dew, I.,

Dietz, S.M.,

Henderson, S.N.,

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COMMENT
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MEDLINE
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weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T.,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye-J., Yeh,R.F.,
Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.,
Zhong,F.N., Zhong,W., Zhou,X., Zhu,X., Smith,H.O.,
Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Muzny, D.M., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, Y., Reese, M.G., Reinert, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden Kiamos, I., Stapleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Venter, F., Wang, A. H., Wang, Y., Wang, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Oct 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z., Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gelbart, W.M., Glasser, K., Glodek, A., Gong, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 303367)
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ann,W., Fosler,C., Gabrielian,A.E., Garg,N.S.,
                                                                                                                                                                                                                                                                                                                                                                                      SEIGNGGKELPTPAAVQERFQRNMRNRCKHQLRSGHRACLEVFRNGYRKCTTNFPSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .303367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorrell, J.H., Gu, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zheng, X.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ferriera, S.,
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PUBMED
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TITLE
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JOURNAL
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ORGANISM
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Best Local
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Damiano, J.S., Stehlik, C., Pio, F., Godzik, A. and Reed, J.C. Clan, a novel human ced-4-like gene Genomics. 75 (1-3), 77-83 (2001)

21365712
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Submitted (21-FEB-2001) Program on Apoptosis and Cell Death
Research, The Burnham Institute, 10901 North Torrey Pines Road,
Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                    Stehlik, C., Damiano, J.S., Pio, F., Godzik, A. and Reed, J.C.
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Mammalia; Eutheria; Primates;
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100.0%;
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CLAN1) mRNA, complete
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BASE COUNT
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AC078439
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GCTGCTGAAGCTGCGGCAGA 819
                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-AUG-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
* NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nixon, J., Morrison, H.G.,
Crocker, M.C., Hinkle, G.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Giardia intestinalis.
Giardia intestinalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAK14778.1"
/db_xref="GI:14324117"
/db_xref="GI:14324117"
/td_xref="GI:14324117"
/translation="MNETKDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCE
/translation="MNETKDNSRALIQRMGMTVIKQITDDLFVWNVLNREEVNIICCE
KVEQDAARGIIHMILKKGSESCNLFLKSLKEWNYPLFQDLNGQSLFHQTSEGDLDDLA
QDLKDLYHTPSFLNFYPJGGEDIOIIFNLKSTFTEPVLWRKDQHHHRVEQLTLVL"
a 157 c 180 g 213 t
                                                                                                                                                                                                                                   /organism="Giardia intestinalis"
/strain="WB-C6"
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1. .865
                                                                                                                                                                                              /db_xref="taxon:5741"
/clone="NJ5017"
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100.0%; Pr
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Best Local S
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Giardia ir
SAMPLING.
                           i (bases 1 to 1198)
Wiener, J.R. and Joklik, W.K.
Comparison of the reovirus serotype 1,2,
encoding the nonstructural protein sigma
Virology 161, 332-339 (1987)
                                                                                                                                                                    M18390.1 GI:333757
sigma-NS nonstructural protein.
Reovirus serotype 2 (strain D5/Jones) viral RNA,
                                                                                                                           Mammalian orthoreovirus
Viruses; dsRNA viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim,U., Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L. Direct Submission
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(bases 1 to 1092)
Morrison, H.G., McArthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.
                                                                                                                                                                                                                                           RNA, complete cds.
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                                                                                                             orthoreoviruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Biology and Evolution, Marine Biological Laboratory, MBL Street, Woods Hole, MA 02543-1015, USA
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Location/Qualifiers
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/clone="KI0936"
270 c 277 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Giardia intestinalis"
/strain="WB-C6"
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Reoviridae;
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                                          serotype 1,2, and protein sigma-NS
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85;
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2 /hases 1
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Rad,M., Rieger,M., Rose,M., Schaaff-Gerstenschlaeger,I., Scherens,B., Schwarzlose,C., Skala,J., Slonimski,P.P., Smits,P.H.M., Souciet,J.L., Steensma,H.Y., Stucka,R., Urrestarazu,A., van der Aart,Q.J., van Dyck,L., Vassarotti,A., Vetter,I., Vierendeels,F., Vissers,S., Wagner,G., de Wergifosse,P., Wolfe,K.H., Zagulski,M., Zimmermann,F.K., Mewes,H.W. and Kleine,K. Complete DNA sequence of yeast chromosome II
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S.cerevisiae chromosome
Z36010 Y13134
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IKTGGFFSCIAMLRPLQYAKRERLLGQRNLERIAARDVLQTRDLHSLCMPTPDAPMTN
YQASTMRELVCDHFKVDHVDGLRYVPMDDRYSPSSLARLFTMGMAGLHITTEPAYKRV
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/db_xref="taxon:10885"
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Feldmann, H., Aigle, M., Aljinovic, G., Andre, B., Baclet, M.C., Barthe, C., Baur, A., Becam, A. M., Biteau, N., Boles, E., Brandt, T., Brendel, M., Brueckner, M., Bussereau, F., Christiansen, C., Contreras, R., Crouzet, M., Cziepluch, C., Demolis, N., Delaveau, T., Doignon, F., Domdey, H., Duesterhus, S., Dubois, E., Dujon, B., El Bakkoury, M., Entian, K.D., Feuermann, M., Fiers, W., Fobo, G. M., Fritz, C., Gassenhuber, H., Glansdorff, N., Goffeau, A., Grivell, L.A., de Haan, M., Hein, C., Herbert, C.J., Hollenberg, C.P., Holmstrom, K., Jacq, C., Jacquet, M., Jauniaux, J.C., Jonniaux, J.L., Kallesoe, T., Kiesau, P., Kirchrath, L., Koetter, P., Korol, S., Liebl, S., Loghe, M., Lohan, A.J.E., Louis, E.J., Li, Z.Y., Maat, M.J., Mallet, L., Koetsen, M., Molemans, F., Mueller, S., Mannhaupt, G., Messenguy, F., Miosga, T., Molemans, F., Mueller, S.,
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Submitted (30-AUG-1994) Data collected by MIPS on behalf of the European yeast chromosome II sequencing project. MIPS at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a D-82152
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                            Martinsried, FRG; E-mail: Mewes@mips.embnet.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Schaaff-Gerstenschlaeger, I. and
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EKWIRSSFENCPGAVALEIGSLSSGNRISRCALFRNVVRIDLEEHEGVIKQDFWERPL
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/chromosome="II"
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d Zimmermann,F.K.
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RESULT 55
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                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 3709)
Benoit,B., Nemeth,A., Aulner,N., Kuhn,U., Simonelig,M., Wahle,
The Drosophila poly(A)-binding protein II is ubiquitous throughout Drosophila development and has the same function in mRNA polyadenylation as its bovine homolg in vitro Nucleic Acids Res. 27 (19), 3771-3778 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rad,M., Rieger,M., Rose,M., Schaaff-Gerstenschlaeger,I., Scherens,B., Schwarzlose,C., Skala,J., Slonimski,P.P., Smits,P.H.M., Souciet,J.L., Steensma,H.Y., Stucka,R., Urrestarazu,A., van der Aart,Q.J., van Dyck,L., Vassarotti,A., Vetter,I., Vierendeels,F., Vissers,S., Wagner,G., de Wergifosse,P., Wolfe,K.H., Zagulski,M., Zimmermann,F.K., Mewes,H.W. and Kleine,K. Complete DNA sequence of yeast chromosome II
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster poly(A)-binding
                                                                                                    and Bourbon, H.M.
                                                                                                                                                                                                                                                                            fruit fly.
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IDDISPVNLPEWTNLAFLSWTILGSLOKLIFLEKETELOKSIFUT IMGGYDVMGKASTG
SGKTLAYGIP IVEKLIS METSOKNIK PLSLIFT PETRELAHQVTDHLKKICGEPULAKSQ
SGKTLAYGIP IVEKLIS METSOKNIK PLSLIFT PETRELAHQVTDHLKKICEFULAKSQ
SKILSLTGGLSIOKQQRLLKYDNSGQIVIATPGRFLELLEKDNTLIKRFSKVNTLILDE
ADRLLQGHFDEFEK IIKHLLWERKHENSEGSSKINGVILTASTFSIDLFINKLSS
RQVKORRFKNERDELANVIQHLMSKIHFNSKPVIIDTNPESKVSSQIKESLIECPPLE
RDLYCYYFLTWFPGTTLIFCNAIDSVKKLTVYLNNLGIPAFQIHSSMTQKNRLKSLER
FKQQSAKQKTINHSNPDSVQLSTVLIASDVAAAGLDIFGVQHYHYHLPRSTDIYIHR
SGRTAARAGSEGVSAMICSPQESMFLKIKKTLATKNSVSTDLNSRSTNKFIKKPKBVSDDIY
VPLLFIETDILSQLRERSRLAGELADHEIASNSLRKDDNWLKKAADELGIDYDSDEDD
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/db_xref="G1:536442"
/db_xref="G1:536442"
/db_xref="G1:536742"
/db_xref="GISS-PROT:P38112"
/translation="MGKKRAPQKGKTVTKPQEIIVDESKLNWKPVDIPDTLDDFGGFY
GLEEIDGVDVKVVDGKVTFVTKKDSKVLKDSNKEKVGDDQESVENESGSDSESELLEF
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ADNLVKKRGHNSIIGHEKTNALETLKKKKKRNN"
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279. .2600
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/db_xref="taxon:4932"
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                                                                                                                                                                               Zagulski,M., Becam,A.M., Grzybowska,E., Lacroute,F., Migdalski,A., Slonimski,P.P., Sokolowska,B. and Herbert,C.J.

The sequence of 12.5 kb from the right arm of chromosome II predicts a new N-terminal sequence for the IRAl protein and reveals two new genes, one of which is a DEAD-box helicase Yeast 10 (9), 1227-1234 (1994)
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                                                                                                                                                                                                                                                                                   Eukaryota; Fung1; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 12595)
                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                             baker's yeast.
                                                                                                                                                                                                                                                                                                                                                                         DEAD box protein; helicase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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Bourbon, H.-M.
                                                                                Submitted (21-APR-1994) C.J. Herbert, Centre de Genetique Moleculaire, CNRS, 91198 Gif-sur-Yvette, FRANCE
                                                                                                                      Direct Submission
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                                                                                                                                      (bases 1 to 12595)
bert, C.J.
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а 777 с
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257. .3226
              /organism="Saccharomyces
/strain="S288C"
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FRGRQIKVMSKRTNRPGLSTINRFARGSFRGRGARVSRACCHSTFRGARRAMGYRGRA
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/chromosome="2"
/db_xref="taxon:4932"
                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAIKARVKEMEEEAEKIKQMQSEVDKQMAGGSTTGLATVPLSLEEKQEIDTRSVYVGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MADEDITLNEDQLLESLEETNGEQETETATEVEEEGSMQIDPEL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="poly(A)-binding protein
/protein_id="AAF00976.1"
/db_xref="GI:6007612"
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join(257. .562
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/strain="Oregon R"
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e (S288C)
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NLDFGTRLHKSBETYVDDDTTFFLALIFKAFSSSSTELTPYINKYMLDGLENDVLPQE
HIPTVVCSLSYWVPNLYEHVYLANDEBGPEAISRIIYSLIRLTVKEPNETTAYLQQIE
FLLALDGRLTNVIVEEIVSHALDRDSENRDWMKAVSILTSFPTTEIACQVIEKLINMI
KSFLJSLAVEASAHSWSELTILSKISVSIFFESPLLSQMYLPEILFAVSILLIDVGPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLISVDVSNTTGVSSEFTLSLDNEEKLVFCSPKYLEIVKMFYYAQLKMEEDFGTDFSN
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SKLKFNTRTLKVLQNMSHHLSGSATISKSSILPDSQEFLQKRNYPAYTEKIDLTIDYI
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ADSVFNSCRSIILNIAITKDLNPIIENTLGLIDLIVQDEEITSDNITDDIAHSILVLL
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/db_xref="GI:547576"
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complement(8728. .9741)
                                                                       SELMKEL"
                                                                                                                     MMILGIMSKSHTSLFLCKELLVETMKVFAEPVVDDEQMFIIIAHVFTYSKIVEGLDPS
                                                                                                                                                                                             FAASSFSSKFGTLDLFTKNIMLLMEYGSISEGAQWEAKYKKYLMDAIFGHRSFFSARA
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SLIKNESKSKDTSDLAVMYTLLGYIMNQINKLGGLETYQIASQNGQLKERGGDTSKLL EKWIRSSFENCPGAVALEIGSLSSGNRISRCALFRNVVRIDLEEHEGVIKQDFMERPL PRNENDKFDLISCSLVLNFVKNHRDRGAMCHRMVKFLKPQGYIFIVLPQACVTHSRYC

DKTLLQNLLGSIGLIMLNSHQSNKLYYCLYQLQVVSPQPSSFSKRIKVNDGPGLNNFG

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/protein\_id="CAA55538.1" /db\_xref="GI:547577"

/codon\_start=

complement(8728. .9741) /gene="YBR1118"

/gene="YBR1118"

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Hum. Mol. 93271985
      Greenspan,D.S.
The carboxyl-terminal half of type VII collagen, including the non-collagenous NC-2 domain and intron/exon organization of the corresponding region of the COL7A1 gene Hum. Mol. Genet. 2 (3), 273-278.(1993)
                                                                                                                                                                                        The large non-collagenous domain (NC-1) of type VII collagen is amino-terminal and chimeric. Homology to cartilage matrix protein, the type III domains of fibronectin and the A domains of von
                                                                                                                                                                                                                                                                       Christiano,A.M., Rosenbaum,L.M., Chu Woodley,D.T., Pan,T.C., Zhang,R.Z.,
                                                                                                                                                                                                                                                                                                                                   Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L23982.1 GI:495865 collagen type VII; intergenic region; structural protein Homo sapiens (tissue library: lambda EMBL3, Lambda FIX) [...]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMCOL7AlX 36631 bp DNA PRI 05-JAN-1995
Homo Sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67)
collagen type VII intergenic region and (COL7A1) gene, comple
                                                                                                                                    93338437
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VPLLPIETDILSQLRERSRLAGELADHEJASNSLRKDDNWLKKAADELGIDVDSDEDD
ISKSNSDTFLLKNKNKKMQKTINKDKVKAMRATLNELLSVPIRKDRQKYLTGGLVNL
ADNLVKKRGHNSIIGHEKTNALETLKKKKKRNN*

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IDDISVULPEWINLAPLSMTILGSLÖNLIKELKERELĞÜKSIEPVI MÜĞÜYDVMĞKASTĞ
SĞKTLAYĞIEPTVEKLISENFSOKIK KPISLIFTETRELAPOVTDHLKKICEPVLAKSQY
SİLSLTĞĞLSİOKQĞRLLKYDNSĞQIV ATPĞRELELLEKDNTLIKRESKVNTLILDE
ADRLLOÐĞHDDEFEKIIKHLLVERRKINENSESSKUMÖTLLESATESIDLFDKLSSS
RÖVKDRREKNNEDELAAVIQHLMSKIHENSKEYPIIDTNPETKVSSÖIKESLIECPPLE
RDLYCYYFLTMEPĞTTLIFCNALDSVKKLTVYLINLĞIPAFQIHSSMTÖKNRLKSLER
FKQÖSAKÖKTINHSNEDSSOLSTVLIASDVAARĞLDIPĞVQHVIHLERSTDIYIHR
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/translation="MGKKRAPQKGKTVTKKPQEIIVDESKLNWKPVDIPDTLDDFGGFY
GLEEIDGVDVKVVDGKVTFVTKKDSKVLKDSNKEKVGDDQESVENESGSDSESELLEF
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Hottman, G.G., Lee, S., Christiano, A.M., Chung-Honet, L.C., Katchman, S., Uitto, J. and Greenspan, D.S. Complete coding sequence, intron/exon organization, and clocation of the gene for the core I protein of human ubiquinol-cytochrome c reductase
J. Biol. Chem. 268 (28), 21113-21119 (1993)
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/db_xref="taxon:9606"
/cell_type="fibroblast"
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/tissue_lb="lambda EMBL3, I
                                                                                                                                                                                                                               /gene="COL7A1"
/bound_moiety="SP1"
3743. .3748
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PSERQEVNVPAGETSVRLRGLRPLTEYQUTVIALYANSIGEAVSGTARTTALEGPELT
IQNTTAHSLLVAMRSVPCATGYRVTWRVLSGGTTQQDEIGPGQGSVLLRDLEPGTDYE
VTVSTLFGRSVGPATSLMARTDASVEGGTTLAPYLIGPTSILLSWLVPEARGYRLEWRR
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SPVTDLQATELPGQRVRYSWSPVPGATQYRIVATLLEGHEWATPATVVPTGPELDVQ
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VTGATAYRLAWGRSEGGPMRHOLIFGNTDASEIRGLEGGVSYSVRVTALVGDREGTPW
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APGLKGSPGLPGRTGAPGPGPGFFGADGRPGSPGRAGNPGTPG
APGLKGSPGLPGFRGDPGERGFPGADGRPGSPGRAGNPGTPG
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Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

EXCEPTION: This sequence is not the entire insert of clone ROIEG. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-NOV-1995) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
sequence 270208. The true left end of clone F54B11 is at 40834 in this sequence. The true right end of clone F18H3 is at 23326 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAV 20-JU
Caenorhabditis elegans cosmid R01E6, complete sequence
268118
                                                                                                   neighbouring submissions.
The true left end of clone R01E6 is at 1 in this sequence. The true right end of clone R01E6 is at 340 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coles,L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z68118.1 GI:1082133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The C.elegans Sequencing Consortium. 2 (bases 1 to 40937)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; Acetylcholine receptor protein; Carbonic anhydrase; Guanylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 40937)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40937 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 9; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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FEATURES
                                                                                                     CDS
                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence Z70208.
For a graphical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z50110.
The end of this
                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ROIB6.5"
/note="cDNA EST yk146b3.5 comes from this gene cDNA EST yk170c5.5 comes from this gene cDNA EST yk170c5.3 comes from this gene cDNA EST yk170c5.3 comes from this gene cDNA EST yk412b8.3 comes from this gene cDNA EST yk412b8.3 comes from this gene cDNA EST yk412b8.5 comes from this gene cDNA EST yk42c1.3 comes from this gene cDNA EST yk42c1.3 comes from this gene cDNA EST yk42c1.3 comes from this gene cDNA EST yk42c1.3 comes from this gene cDNA EST yk42c1.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="R01E6.4"
join(999. 1127,
1958. 2060,2118
                                                                                                                                                                  /db_xref="Sptrembl:Q21616"
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YSQDGKAADHDALHKDAAKYAGDEHNAGQQHKDNGGYHADGHQGYDKAQKTKGFFDYRY
VQPQYHMEQYHTDEKHANKYAGDEHNAGQQHKDNGGYHADGHQGYDKACKTKGYBHTN
YGNEDAGHKSKYDDNEGKYGDHTDGYYNKGYDNYGQGHDSESYQPSYYQPKPKYYGGH
QSHYQPSARHSSPYQGDQYYGYEAPHY"
QSHYQPSARHSSPYQGDQYYGYEAPHY"
1014 1114 11169 11105 111215 111321 111420,11472 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRPVKNSSDILTVDVGASLIRIIDVDEKNQVLTTNLWLEMKWNDAKLTWTPEKYGGLK
TLHIBSDFIWTEDLVLINNAAGDPDITILTDALVTFEGNVYWQPBAIYKSFCPIDVTW
TLHIBSDFIWTEDLVLINNAAGDPDITILTDALVTFEGNVYWQPBAIYKSFCPIDVTW
FPYDSQKCEMKEGTWIYTGRYVDLKQLPQEEVVITIKYDDUEFWQQMDLSFFYRSA
EWDLLSLTSERHSVLXSCGGPEKYVDITYYFGLRRKTLFFTCNLILPGFLISILTTF
VFYLSDHKITESISILVTLTVFFLVLLDLMPPTSLVIPWFGRYLLTTMILVALSTYVS
VITVNFRFRSGSAHKMSPWIRAVFLKFLPKILLMSRPEKGEVTKQPPLVNAASLVGSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA ES
                              /gene="R01E6.3"
/note="~
                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/protein_id="CAA92185.1"
/db_xref="GI:3878770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAQNNNAPTVAFRKTKRQKSKSVDDVVFMNLLNQVRFIAEHFRHNELEGEISDDWTFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA92184.1"
/db_xref="GI:3878769"
/db_xref="SFTRMBL:021615"
/translation="MESENWALILLVAVGGTNAFKIKRTAKDLESQLYEDLLFDYNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Neurotransmitter-gated ion-channel), Score=484.8, E-value=2.2e-142, N=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="R01E6.5"
join(5029. .505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMVLDRLFLIIFSVLNVGTVFIILESPSLYDYSKPMNITVPNKPLGQANFYSSWNLK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YATAAKAANEYRNKAKGKNNDLMSLRGKPSSQAVLNNTFDMRMRNNDSTVENRLKPYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(999.
1958. .20
                           note="contains"
                                                                                                                       /gene="R01E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(5029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="contains similarity to Pfam domain: PF00065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="R01E6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
  Eukaryotic-type
                                                                                                   oin(11014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="R01E6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .40937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST yk268h8.3 comes from this gene EST yk268h8.5 comes from this gene EST yk354e9.3 comes from this gene EST yk354e9.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                999. .1127,1467. .1589,1647. .1756,1803. .1905, .2060,2118. .2307,2362. .2503,2557. .2747,3149. .3441,3489. .3656,4047. .4244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99. .1127,1467. .1589,1647. .1756,1803. .1905,
.2060,2118. .2307,2362. .2503,2557. .2747,3149.
.3441,3489. .3656,4047. .4244)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence (40834. .40937) overlaps with the
                                                                                                                                                 .12167,12215.
                                                                       12167,12215
                                                                                                                                                                                                                                                                                                                                                                                                                         yk309d12.3 comes
yk309d12.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5054,5131. .5546,5594. .5889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5054,5131. .5546,5594.
  similarity
e carbonic a
                                                                                                                                                      .12304)
y to Pfam dor
anhydrase),
                                                                                                   .11235,11321.
                                                                                                                                                                                                                                                                                                                                                                                                                         this
this
                         domain:
                                                                                                                                                                                                                                                                                                                                                                                                                       gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 5889)
                                                                                                   .11420,11472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                           PF00194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         start of
                                                                                                                                                                          .11686,
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21729. .
23999. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPDDCVAKSSCVNYIPHIIAAVVIVTIIVIAIVIIVKQRRHKLNIYKLTWKVPKESLK
IIVNKNADAKWQRELEKRASNTDNAAALTSRRFVEGSYALVGTGRAEYVQFKQIKKIN
FPETTLDYLYSLKQLQHDNLAKFYGIQVNDDITMTILTILVERGTLEEFCLDRDFGM
DDTFKSAFMRDILKGLQYLHKSSIGYHGHLQASTCLLDINWVLKLTLYVSVNFWSDQL
DAENIKVPEQAAHMITYPQYVCFPPEHIREYDDSGKQPPRVVRGSPKGDIYCVGMIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(13219...13506,13552...13698,13747...1381)
13862...13985,14486...14626,14675...14843,14895...15086,
15323...15497,15549...15620,15673...15963,16018...16099,
16292...16364,16408...16501,16800...16951,17049...17172,
17430...17501,17549...17721,17789...17885,17932...18006,
18054...18420,18589...18656))
//gene="ROILEGIT"
                                                                                                                                                                                                                                                                                                                                                                                               complement(join(20486.
21729. .21881,22959. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKNYKLRIRIGFHAGPIAAGVIGIRSPRYCLFGDTVNFASRMQSNCPPNQIQTSEITARLLFDSHEYKFVKRGIVHVKGKGNAARLKICCETFETHSIDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLNEMLPASIAKDLKNGLIMPPRSYESATVMFVQICDFNALMKRSSPEQVIAFLNDIY
DQFDTVIKRHDAYKVETTGETYMVASGVPHENEGRHIFEVAEISLEIREISYIYVLQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMVEREDPYHLTHSVERPNATLIKQTLNENHMPRITDDYRQENMLLEMCKECWDRNPD
KRPTIKKLIESISTVYPLSKGNLVDQMIRMSEKYADELEQMVAIRTADLADAQMQTMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYEPVFEARGVQELTSVINVAQFSVGGVAETLVFLMKELEQVEITLVGSVKVLPNGLS
LSNDLRSYNEIMNSFKIREYVBVDENNDYMTKVDQKIKRGARMIVVCADFYDIYSAFY
NIGITRSLSGFRFIIVVLINKPPDEILNQPNVKNLLYGSNAFIISPLQEVSDAFSIDD
DVIPNLADDQFTTFLRIYHACYAYCVGSVNGAETQTDNYHTAMSGKAVTTKYGTTFED
NSGSVLTNYAVFTINPAEMTFESILTLKSVAKSCDTYNCFQLSPNKTSDLLWTLKDMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA92186.2"
/db_xref="G1:14530534"
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/trans1ation="MCYLRLWOMRRPMDSVQQSQYSEKHLELLTVIILLKLFGVFHRI
/trans1ation="MCYLRLWOMRRPMDSVQQSQYSEKHLELLTVIILLKLFGVFHRI
NQQHGCSGDNSVKSASYAINAVASRTSGELDFVFVGPTCTTDIRTIGDFAEIWKSPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains similarity to Pfam domain: PF00069 /note="contains similarity to Pfam domain: PF00069 (Eukaryotic protein kinase domain), Score=25.7, E-value=1.6e-06, N=2; PF00211 (Adenylate and Guanylate cyclase catalytic domain), Score=191.2, E-value=5.5e-54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(13219. .13506,13552. .13698,13747. .1381
13862. .13985,14486. .14628,14675. .14843,14895. .15086,
15323. .15497,15549. .15620,15673. .15963,16018. .16099,
16292. .16364,16408. .16501,16800. .16951,17049. .17172,
17430. .17501,17549. .17721,17789. .17885,17932. .18006,
18054. .18420,18589. .18656))
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TDVCKADALNIDYKSGDCCDVLVSEGGFLVNVKRNCGTFLTANHLPSSKFALAQFHAH
WGSNSKEGSEHFLDGKOLSGEVHFVFWNTSYESFNVALSKPDGLAVVGVFLKEGKYND
KSSRMSTSTASNTSRQKSITSIKDKDRPKSSRESKNIEISRTKSMRKDSHPISAQGRE
IITQCFENPHSEFANKVVQRIFEKREDYQKYIMNLGKERSSIVNNRLKQLVEDIVAHI
                                                                   /protein_id="CAA92187.1"
/db_xref="G1:3878772"
/db_xref="G1:3878772"
/translation="MGNSSSSSSRINKKSESMEIRSKPNRSSVSGEFNKSKSMMDMSS
                                                                                                                                                                                                                                                                                       /gene="R01E6.6"
/note="similar to 951004:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFTEPVEVSFGQLNVLRNIIPANHRACQDRCDREIRSSFNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYHGLIDTVRKATGNATPIAMPKDFHIEHLLPSPDKREFVTYLGSLTTPPYNECVIWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-value=8e-40, N=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="R01E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23999
                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="R01E6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:Q21614"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:3878775"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA92190.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A EST yk202f1.3 comes 1
A EST yk202f1.5 comes 1
A EST yk234h4.3 comes 1
A EST yk234h4.5 comes 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ement(join(20486. .20551,21018. .21101,21336. .2149
. .21881,22959. .23081,23639. .23753,23802. .23950,
                                                                                                                                                                                                                                                                                                                                                          24088))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Caenorhabditis briggsae
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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Submitted (04-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6:
Submitted by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University Genome Sequencing Center.
The C. briggsae Genome Sequencing Project
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                                                                                                                                                                                          /organism="Caenorhabditis briggsae"
/strain="GujArat G16"
/db_xref="taxon:6238"
/clone="G39N14"
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PLSPHHIPANEMYLTLLQRLLQAAQPDARSSNNL"
complement(join(33511. .33756,33804. .33947,33995. .34096,
34158. .34242,34362. .34369))
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/gene="R01E6.2"
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/db_xref="GI:3878773"
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Direct Submission
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Street, Waltham, MA 021
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                                                                                              Smith, D.R.
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 45459: contig of 45459 bp in length.
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                                                                                                                                                                             Note: Clone was sequenced in 1996 using Multiplex DNA Sequencing Technology. Data may contain low quality seq uence and BAC/Cosmid vector sequences.
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/chromosome="10"
/map="10q25.1"
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/db_xref="taxon:9606"
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                                                                                                                                                            corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL159169
Human DNA
                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk
On Aug 29, 2000 this sequence version replaced gi:9908927.
During sequence assembly data is compared from overlapping clones
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Thiwas generated from part of bacterial clone contigs of
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20; Conserv
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                                                                               The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                         annotated human repeat sequence elements (e.g. Alu). sequence is ambiguous, there is an annotation using
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Submitted (02-MAR-1999) Ger
Street, Waltham, MA 02154,
5 (bases 1 to 83969)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission Submitted (11-DEC-1998) Genome Therapeutics Corporation, 100 Beaver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 83969)
Smith, D.R.
                                                                                                                       feature key.
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/db_xref="taxon:9606"
/chromosome="10"
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Eutheria; Primates;
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19036 c 18255 g 22298 t
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP11-408A13
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76;
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This sequence of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP11-408A13 It may be shorter because we sequence overlappin sections only once, except for a 100 base overlap. The true right end of clone RP11-408A13 is at 86155 in this sequence. The true left end of clone RP11-439N12 is at 95 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HBP/Chr9 RPI1-408A13 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence. The true right end of clone RP11-120J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR
1112. .1245
                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 3. 9777 .10318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER5A repeat: matches 3. 5103. .5207
                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER5A repeat: matches 9.
7190. .7282
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MER5A repeat: matches 65. .166 of consensus" 5132. .5233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1..92)
/note="match: GSS: Em:AQ351225"
104..499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2745. .3053
/note="AluSg repeat: matches 1. .309 of 3152. .3341
                                                                                                                                 /note="match: GSS: 14510. .15126
                                                                                                                                                                                                              10804.
                                                                                                                                                                                                                                                  complement(10404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1M4 repeat: matches 4699.
1511. .2117
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                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ395702"
complement(10404. .10831)
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                                     'note="match:
                                                                         'note="MIR repeat:
                                                                                                                                                                                                                                note="match: GSS:
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1708. .4847
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                                                                                                                                                                                        'note="MIR repeat: matches 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="MIR repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="106 copies 2 mer tt 55% conserved"
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                                                                                                                                                                                                                                                                                                                                             repeat: matches 2577.
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                                 GSS: Em:AQ394111"
                                                                                                               GSS:
matches 2680.
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                                                                         matches 66. .256
                                                                                                             Em: AQ310218"
                                                                                                                                                    Em: AQ665295"
                                                                                                                                                                                                                              Em: AQ030903"
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is at 100 in
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28834. 29034
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23323. .23412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MSTB-internal repeat: matches 1. .1651 of consensus"
37465. .37675
/note="MSTB repeat: matches 203. .420 of consensus"
37685. .37913
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35486. .35885
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33146. .33212
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32743. .32817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: GSS: 30938. .31350
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29795. .30640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1M4 repeat: matches 3018.
29792. .30537
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                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2642.
43215. .43505
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29035. .302
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24826. .24898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="15 copies 2 mer ga 93% conserved"
20263. .20342
                                                                                                                                              /note="AluJb repeat: matches 3.
46261. .46675
                                                                                                                                                                                                                                                                                                                                                                                                 42168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="24 copies 2 mer tt 75% conserved"
40066. .40259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MSTB repeat: matches 1. .229 of consensus"
39397. .39444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"MSTB repeat: matches 1. .426 of consensus"
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                                   /note="L2 repeat: matches 1181. .2181 of consensus"
48487. .48532
                                                                                                                           /note="HAL1
                                                                                                                                                                                                /note="MIR repeat: matches 4.
                                                                                                                                                                                                                                    'note="L2 repeat: matches 2264. .2709 of consensus'
                                                                                                                                                                                                                                                                   note="MIR repeat: matches 216.
                                                                                                                                                                                                                                                                                                         'note="L2 repeat: matches 2696.
                                                                                                                                                                                                                                                                                                                                         /note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                              /note="20 copies 2 mer aa 82% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L1M4 repeat: matches 4385. .4593 of consensus"
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                                                                   19 copies 2
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                                                                                         aa
                                                                                         81%
                  76% conserved"
                                                                                       conserved"
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KEYWORDS
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Local Similarity 100.0%; Nes 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens genomic DNA, chromosome region, complete sequence. Ap000885
                                                                                                                                                                                                                                   Direct Submission
Submitted (15-DEC-1999) to the DDBJ/EMBL/GenBank databases.
Submitted (15-DEC-1999) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC): Kitasato Univ., 1-15-1
Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
 Similarity 20; Conserv
                                                                                                                                                                                                                                                                                                                                                        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 86,719 genomic DNA of 21922.1

Published Only in DataBase (1999) In press
2 (bases 1 to 86719)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Conservative
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/map="21q22.1"
a 16034 c 16025
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48824.49187
/note="THEIC repeat: matches 1. 371 of consensus"
49538..49616
/note="MER588 repeat: matches 275. .336 of consens.
08617..40672
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/note="MIR repeat:
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54014..54039
/note="13 copies 2 mer ca 100% conserved"
54903..54981
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50459. .50934
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50230. .50439
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/note="LIMB2 repeat: matches 5810. .6163 of
                                                                                                                                                      /db_xref="taxon:9606"
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                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                      Location/Qualifiers
               0.6%;
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                 Score 20;
Pred. No.
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CATAGTCAAGTCTCTGTCAA 3128
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KEYWORDS SOURCE ORGANISM RESULT AC005923 VERSION ACCESSION DEFINITION EFERENCE AUTHORS Culpepper, Ding, Y. Dugan, S.P. Durbin, K.J., Forcum, J., Ganesh, R.P., Garcia, C., Garcia, D.K., Gorrell, H., Gorrell, L.L., He, X., Hernandez, J., Jackson, L.E., Kondejewski, N., Leal, B., Lichtarge, O., Liu, W., Logan, O., Lu, J., Martinez, C., Moore, S., Moorish, T., Ngyuen, N., Oswal, G., Pampell, L.R., Parish, B.J., Perez, L.M., Rashid, N.D., Rives, C.M., Scherer, S.E., Shen, H., Simon, M.L., Vo, Q.K., Weit, Y., Williamson, A.L., Worley, K., Zhou, Naylor, S.L. and Gibbs, R.A. Mammalia; Eutheria; P 1 (bases 1 to 88326) Muzny, D., Arenson, A.D., Bouck, J., Bunac, C., AC005923 88326 bp DNA PRI 12-JAN-2000 Homo sapiens 3p21.3-4 PAC RP4-751E10 (Roswell Park Cancer Institute AC005923.2 GI:4309927 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Human PAC Library) complete sequence Chen, J., Chen, Z.,

, L.L.,

REFERENCE AUTHORS TITLE JOURNAL JOURNAL Worley, K.C.
Direct Submission Unpublished 1 to 88326)

REFERENCE AUTHORS REFERENCE TITLE AUTHORS JOURNAL Submitted (27-FEB-1999) Human Genome Sequencing Center, Departed Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA Submitted (04-NOV-1998) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 88326) Direct Submission Worley, K.C Department

EFERENCE AUTHORS TITLE of Molecular and Human Baylor Plaza, Houston, 5 (bases 1 to 88326) Submitted (12-MAR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

TITLE JOURNAL

Worley, K.C

(bases 1 to 88326)

Direct Submission

Submitted (12-JAN-2000) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Mar 1, 1999 this sequence version replaced gi:4033655.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Worley, K.C. Direct Submission Department

COMMENT

gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. only

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome of a local database that includes entries local mapping efforts. Res. 7:541-550) searches from dbSTS, GDB, and

flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar. Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and CDMA sequences. Genes demonstrate at least two exons

> SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguittes or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguittes. If the sequence quality for a region does not meet this standard, it will be indicated in the a region does not meet this annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality info/monhanhi http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

FEATURES misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region source repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region QUALSTAT - REPORT /rpt\_family="L2" 4833. .5049 /rpt\_ 1009 /note="Region: Clone qk32c09.x1 Homo sapiens cDNA AI245778" /rpt\_family="L2" 4182. .4486 /rpt complement(3554. complement(3407 complement(3262 complement(2651 /rpt\_ /rpt\_ /rpt\_family="7SLRNA" 1431. .1728 /rpt\_family="AluJb" 1299. .1327 /rpt\_family="L1ME" complement(877. .9 complement(380. complement(4023 complement(3806. /rpt\_family="Alusx"
complement/21^2 /rpt\_family="AluSx"
complement/corr /rpt\_family="L1M4"
complement/con complement(2356. complement(2104. complement(684. complement(1, .61) /rpt\_family="AluY" /rpt\_family="AluSq" /rpt\_family="AluJo" /rpt\_family=" /rpt\_family=" /rpt\_family="AluSc" rpt\_family="AT\_rich" /rpt\_family="L1ME" /rpt\_family="Alu" /clone="RPCI5-751E10" /db\_xref="taxon:9606" /organism="Homo sapiens" location/Qualifiers \_\_family="AluSx" lement(60' \_family="Aluy"
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Caenorhabditis briggsae
                                                                                                                                         20;
                                                                                                                                                       Similarity
                                                                                                                                         Conservative
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47716. 47800
/note-"Sequence is generated
/function-"low coverage"
47802. 48101
47802. 48101
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/note="Region: Homo sapiens CpG island DNA genomic
fragment 258606"
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/rpt_family="(GA)n"
complement(31427. .31535)
/rpt_family="L2"
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complement(48158. .48460)
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complement//
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complement//7:00
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/note="Region: Similar to Human mRNA for KIAA0279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Unigene cluster containing AA057543 and AA411587"
/standard_name="D3S4222"
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/gene="Unigene cluster containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="L2"
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'gene="Unigene cluster containing AA057543 and AA4115

'4592. .44724
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6. .47800
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Pred. No. 76;
cosmid CB019G12,
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                                                                                                                                         0;
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                                         Direct Submission
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                                                                                                              Homo sapiens
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Db 67631 AGGTCCCACAACTCGTCAAG 67612
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AL391278.10 GI:12331116
HTG; HTGS_PHASE1; HTGS_CANCELLED
Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                 AL391278 91733 bp DNA
Homo sapiens chromosome 1 clone RP5-885P2,
PROGRESS ***, 29 unordered pieces.
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91733)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (04-NOV-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 88839)
Washington University Genome Sequencing Center
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Caenorhabditis briggsae
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Department of Genetics, Washington
St. Louis, MO 63110, USA
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/product="tRNA-Gly"
16056 c 16645 g 28058 t
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/product="tRNA-Pro"
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/strain="GujArat G16"
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 2 coverage: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be preserved.
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         2 60711: gap of 10
2 63058: contig of 2
9 63158: gap of 10
9 65257: contig of 1
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7 30171: contig of
2 30271: gap of
2 32949: contig of
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57401: contig of 3288 b
57501: gap of
60631
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                                                                                                                                        49339: contig of 2123 bp in
49439: gap of 100 bp
54013: contig of 4574 bp in
                                                                                                                                                                                                          41583: gap of 100 bp
44333: contig of 2750 k
44433: gap of 100 bp
47116: contig of 2683 k
                                                                                                                                                                                                                                                                    33049: gap of 100 bp 36523: contig of 3474 bp in length 36623: gap of 100 bp 38651: contig of 2028 bp in length 38751: gap of 100 bp 41483: contig of 2732 bp in length 41483: contig of 2732 bp in length
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36523: con
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49339: cont
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15825: con
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17982: contig of 2057 k
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87563 91733: contig of 4171 bp in length
Location/Qualifiers
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/note="assembly_fragment:00329"
30272. .32949
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63159. .65257
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57502. .60611
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38752. .41483
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24495. .27186
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                       /note="assembly_fragment:00677"
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49440. .54013
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              'note="assembly_fragment:00835
                                            note="assembly_fragment:00805"
                                                                           note="assembly_fragment:00758"
                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:00476"
                                                                                                                                                                                                                                                                                                                              38752. .41483
'note="assembly_fragment:00437"
                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment:00337"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:00334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment:00196'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:00136"
12887. .15825
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fragment_chain:1"
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80699: contig of 5112 bp
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84813: contig of 4014 bp
813: gap of 100 bp
87462: contig of 2549 bp
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854: gap of 100 bp
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JOURNAL REFERENCE
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AUTHORS
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ORGANISM
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AC073294
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          Center:
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Submitted (13-JUN-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                          -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 93409)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing of Mouse
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                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the prices is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 93409: contig of 93409 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ordered pieces
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/note="assembly_fragment:00938"
84914. .87462
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18159 c 18530 g
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75588. .80699
                                                                      /clone_lib="CitbCJ7 mouse 21194 c 20677 g 25391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 to 93409)
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                                                                                                     /clone="CT7-32I19"
                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                    /strain="129 SV"
                                                                                                                                                  /organism="Mus musculus"
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Score 20;
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985 othe
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            Length 93409;
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94598, US
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AUTHORS
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AC083819/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metzker M.L., Lewis,L.R., Hume,J., Euwarus,C., Garner,T., Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T., Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J., Chacko,J., Chen,G., Chen,Z., Bunhav,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z.,
                                                     * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tnc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G. Worley,K. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cox,C. Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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PROGRESS ***, 7 unordered pieces.
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as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 95179 bases at least Q40
Consensus quality: 98007 bases at least Q20
Consensus quality: 99497 bases at least Q20
Consensus quality: 99497 bases at least Q20
Consensus quality: 99497 bases; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
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les 20; Consert
                                                      The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                              This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the
                                                                                                                                                                                                                                                                                                                              together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
On Nov 23, 2000 this sequence version replaced gi:11225761.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 106601)
                    Group. Further information can be found http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                sequence is ambiguous, there is an annotation
                                                                                                                                                                                                                                                                                                                only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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/chromosome="1"
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IMPORTANT: This sequence is not the entire insert of
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                                                                                                                                         /note="MIR repeat: matches 87. 29675. .30120
                                                                                                                                                                                                                                                                                                                                                        15675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="3 copies 15
13996. .1427°
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13942. .13995
/note="18 copies 3 mer tta
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                                                                                                                                                                              /note="MER5A repeat: matches 47. .182 of consensus"
29307. .29439
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                                    33081.
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12435. .12545
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10378. .10458
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11644. .11807
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/note="L1PA12 repeat:
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/db_xref="taxon:9606"
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/note="L2 repeat: matches 2608.
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                GSS: Em:AQ783759"
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47890. 480//
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46829. .47635
                                                                                                                                                                                                                                   /note="L2 52009. .5:
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51027. .51334
                                                                                                                                                                                                                                                                                                                                                                                          /note="LIM4 repeat: 49813. .50122
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                 /note="MER57B repeat: matches 1.
55697. .56012
                                                                                                           /note-"LlPA7
53493. .5415
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                                                                                                                                                                                                                                                                                               /note="AluY repeat: matches 1. .308 of consensus"
51368   .51496
                                                                                                                                                                                                                                                                                                                                                             /note≃"AluSq repeat: matches 1.
50653. .50930
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47842. .4788
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                                                                                                                                                                                                                                                                  /note="L1PA10 repeat: matches 6029. .6156 of consensus"
51510. .51947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46385.
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46036. .46436
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44201. .44518
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42175. .42385
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35174. .35517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1PA3 repeat: matches 6048.
35092. .35173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MIR repeat: matches 4. .165
34988. .35085
/note="AluSc repeat: matches 1.
                                                                             /note="match: GSS: 53511. .53921
                                                                                                                                          52519
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1P repeat: matches 3526. .3683 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="24 copies 2 mer ta 97% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="match:
45984. .46189
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                                                               note="match: GSS: Em:AQ011862"
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                                                                                                                                                                                                                   /note="45 copies 2 mer ga 84% conserved"
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                                                                                                                                                                                                                                                 repeat: matches 1292. .1752 of consensus"
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 .305 of consensus"
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                                                                                                                                                                                                                                                                             regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: RMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP databases can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALL39036 109810 bp DNA PRI 26-MAN Human DNA sequence from clone RP11-285H24 on chromosome 13922.1-22.3, complete sequence.
                                                                                                             http://www.sanger.ac.uk/HGP/Chr13
RP11-285H24 is from the library RPCI-11.1 constructed
of Pieter de Jong. For further details see
                                                                                                                                                                                 was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                requests: clonerequest@sanger.ac.uk
On May 31, 2001 this sequence version replaced gi:14269884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-MAY-2001) Sanger Centre, Hinxton, Cambridgesh CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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AL139036.12
                      RP11-285H24 It may
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IMPORTANT: This :
                                                                                         http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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57865. .58157
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                   This sequence is not the entire insert of clone I I may be shorter because we sequence overlapp
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except for a 100 base overlap
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                                                                                                                                         by the group
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complement(6237..6 complement(1. .98)
/note="match: GSS: Em:AQ374965" complement(18803 complement(9052 complement(6380 /note="MIR repeat: matches 12.
complement(6151. .6886) /note="match: GSS: Em:AZ374306" 11196. .11815 /note="LlM4 repeat: matches 4013. .4108 of consensus" note="MIR repeat: matches 11. .252 of consensus" /note="match: GSS: Em:AQ801630" 20484. .20699 /note="AluJb note="match: GSS: Em:AZ516011" note="L1ME3A repeat: matches 6016. .1190. .11776 Toote="AluSx repeat: matches 1..284 of consensus" 9905. 10103 9905. 10103 repeat: matches 1..210 of consensus" 10116. 10217 'note="match: GSS: Em:AQ620944" /note="18 copies 2 mer tt 80% conserved" 'note="MIR repeat: matches 60. 'note="HALl repeat: matches 669. note="match: GSS: 0817. 4088 note="16 copies 17 mer 59% conserved" /clone="RP11-285H24" /clone\_lib="RPCI-11.1" Location/Qualifiers note="match: GSS: Em:AQ384942" note="AluY 'note="MIR repeat: matches 12. note="match: GSS: Em:AZ374726" 'note="match: GSS: Em:AQ581403" note="7 copies 27 mer 66% conserved" 1773. .4126 note="59 copies 6 mer ggggga 54% conserved" note="MLT1H repeat: matches 409. organism="Homo sapiens" ob\_xref="taxon:9606" note="7 'note≖"MLT1D repeat: matches 1. note="match: GSS: Em:AQ477479" 718. .3197 note="MLT1H repeat: matches 81. note="match: GSS: Em:AQ092767" . .18991 .8683 .4076 .5248 .3940 .15963 . 6699 .3032 .18878 .13554 .18864 copies 37 mer 63% conserved" repeat: matches 1. repeat: matches 3. .6883) .6889 Em: AQ283095" Em: AZ519175" .168 .306 .220 of consensus" .248 of . 306 .746 of .502 of .189 of consensus" .510 of 0 f of consensus" .6116 of consensus" of consensus" consensus" consensus" consensus" consensus" consensus" misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature repeat\_region misc\_feature repeat\_region repeat\_region repeat\_region /note="MIR repeat: matches 2. .91 26142. .26439 /note="AluSar repeat: matches 3. .3 27548. .27704 complement(24264 . .24689) /note="match: GSS: Em:AQ451631" 24793 . .24874 23477. .23773 /note="AluY repeat: matches 1. 23774. .24043 /note="AluSx repeat: matches 1. .312 of consensus" 51288. .51497 /note="match: 19836. .50027 /note="2 copies 27 mer 94% conserved" 37728. 37913 /note="MIR repeat: matches 100. 32359. .32560 /note="L1MC/D repeat: 50250. .50567 /note="MIR repeat: Ynote="MER63A repeat: matches 1. .210 of 88654. .38727 Ynote="2 copies 37 mer 100% conserved" 19086. .39226 34308. .34780 /note="L1MA8 repeat: matches 5785. 33902. .33951 note="25 copies 2 mer at 74% conserved" 'note="MER2 repeat: matches 1. 'note="MIR repeat: matches 24. note="L1MC/D repeat: i9564. .39981
note="MLTIC repeat: matches 17. .466 of consensus" 9258. .39424 note="MER5B repeat: matches 2. note="MER5B repeat: matches 29. .158 of consensus" 'note="AluY note="match: GSS: Em:AQ064667" 33458. .33489 note="16 copies 2 'note="L1M4 repeat: matches 5518. .5905 of consensus" 33290. .33388 note="AluJo repeat: matches 1. 'note="L1M4 repeat: matches 5318. .5518 of consensus" note="MER2 repeat: matches 4. .345 of consensus" 'note="MER33 repeat: matches 22. note="MIR repeat: matches 67. 15008. .25518 /note="L1ME3 repeat: matches 5861. /note="L1M4 repeat: matches
24092. .24357 note="L1ME3A repeat: matches 6029. .6129 note="match: GSS: Em:AQ517147" e="MIR repeat: matches 12. .111 of consensus"
0. .31675 .50326 .35684 .37308 .37104 .28031 .25698 .52231 repeat: matches 1. GSS: Em: AQ169074" matches 81. mer aa 100% conserved matches 5611. matches 5436. 4107. . 296 .209 of consensus" . 252 .260 of consensus" . 145 .299 of consensus" .172 of consensus" .296 of consensus .261 of consensus" .307 of consensus" .166 of consensus" οf .6288 .4379 .6131 of consensus 0f of consensus"  $\mathsf{of}$ .5813 of consensus" .5813 of consensus" consensus" consensus" consensus" of consensus" of consensus" of consensus" consensus"

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RESULT 72
AC022124/c
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ACO10902
ACO10902.4 GI:104447
                                                          AAAGTCTTTTTCATCAGACA 74172
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Direct Submission
Submitted (25-SEP-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
 AC022124
                                                                                                                                                                                                                                               On Sep 30, 2000 this sequence version Center project name: H_NH0549J07.
                                                                                                                                                                                                                                                                                   Submitted (25-MAR-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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53123. .53421
/note="AluSg1 repeat: matches 1. .299 of consensus"
54142. .54423
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/db_xref="taxon:9606"
/clone="RP11-549J7"
22524 c 23021 g 3423
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Local Similarity
Direct Submission
Direct Submission
Separation Sequencing Facility,
Submitted (03-AUG-1999) Production Sequencing Facility,
Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mi
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277276.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                   Homo sapiens chromosome
AC008390
AC008390.7 GI:11908269
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DOE Joint Genome Institute and Stanford Human
                                                                               2 (bases 1 to 121931)
DOE Joint Genome Institute.
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 121931)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Quality: Phrap Quality >=40 99.7% of Sequence;
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2075G19"
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Direct Submission
Submitted (11-SEP-1999) Multimegabase Sequencing
Submitted (12-SEP-1999) Multimegabase Sequencing
Submitted (11-SEP-1999) Multimegabase Sequencing
                                                                                                                              Submitted (19-NOV-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA On NOV 19, 1999 this sequence version replaced gi:6114900.
                                                                                                                                                                                                                       Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
                                                                                                                                                                                                                                                                                   of Washington, PO BOX 357730, 3 (bases 1 to 124347)
                                                                                                                                                                                                                                                                                                                                                         Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Harrison,G., James,R., Lasky,S., Madan,A., Ratcliffe,A., Shaffer,T. and Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T.
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On Dec 20, 2000 this sequence version replaced gi:7711258.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                             and Hood,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing of human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene, partial cds; and unknown gene, ACO10072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.2. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 121931) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                    Center: Multimegabase Sequencing Center
Center code: UWMSC
Web site: http://chroma.mbt.washington.edu/msg_www
                     Contact: leerowen@u.washington.edu
   Sequencing
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/db_xref="taxon:9606"
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                                    /note="217314:
/replace="c"
117633
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/db_xref="GI:6453844"
/translation="MRPADLLQLVLLLDLPRDLGGMGCSSPPCECHQEEDFRVTCKDIORIPS.PPSTCTL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **Translation="MLGRYREYSNGQAGAIEHLKESLEOSIDQLRSQRLLRNSGGRSI
SVTSLSASDLDGGTGSELHFFPTSPLKDYGDPQGIKRNRSRTGVRFVQETDDMTQLH
GFHQSLRDLSSEQIRLDDFNRELSRRSRSDAETKRALEELTEKLNEAQKQEVFFVKS
LGKVKIQCLSSAEVDNVFPINVWQCGI"
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/notce Intron-exon boundaries defined in relation to EST AI554064. the closest BLASTX similarity is to a
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/note="This clone overlaps RP11-114N19, Accession
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          Waterston, R.H.
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                                          The sequence of Homo sapiens PAC clone RP4-530J23
                                                    Harmon, G., Langston, Y.
                                                                          99063792
                                                                                    Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Sulston, J.E. and Waterston, R.
                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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University, 4444 Forest
5 (bases 1 to 129837)
                                                                                                                                                                                               Submitted (21-DEC-1999) Depar University, 4444 Forest Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                         On Mar 1, 1999 this sequence version replaced gi:3213168.
                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 129837)
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_DJ0530J23
                                                                                                   Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                             Web site: http://genome.wustl.edu/gsc
                                                                                                                                             ----- Genome Center
                                                                                                                                                                                               Department of Genetics, Washington Park Avenue, St. Louis, Missouri 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Mashington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc.

(http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong. VECTOR: pcypAC2
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is GS1-67A24, 200 bp overlap. Actual start of this clone is at base position 1 of RP4-530J23;

actual end is at 7592 of GS1-67A24.

Location/Qualifiers
1. 129837

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1. 1172

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repeat\_region 1542. 1962

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Search completed: March 25, 2002, 19:03:19 
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US-08-870-518-34
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Best Local :
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                                                                                                                                                      GENERAL INFORMATION:
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LENGTH: 1094 base pairs
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APPLICATION NITHTON
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                                                       CORRESPONDENCE ADDRESS:
                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                  APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/870, FILING DATE: 06-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/019,219
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Davis, Roger J.

APPLICANT: Galcheva-Gargova, Zoya
TITLE OF INVENTION: NON-ACTIVATED RECEPTOR COMPLEX
TITLE OF INVENTION: PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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                                                                                                                                                                                                                                                                                       766 ttttccttcttgatggct 783
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TELEFAX: 200154
ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fasse, Peter J.
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No. 6063610el Carboxylesterase Nucleic Acid
Molecules, Proteins and Uses Thereof
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: No. 60636
CLASSIFICATION: 435
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                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
                                                                                                                                                                                                    ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CCITY: Fort Collins
                                                                                                                          MEDIUM TYPE:
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ZIP: 80525
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STRANDEDNESS: sing
TOPOLOGY: linear
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Molecules, Proteins and Uses Thereof
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                                              US/08/747,221B
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Pred. No.
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46;
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NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459

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us-09-005-051-16/c
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Patent No. 6291222
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                              TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 16:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1153 CTCCAAATTCAGAAATCC 1170
                                                                                                                                                                               NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1515 nucleotides
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
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APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1002 ctccaaattcagaaatcc 1019
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                  FEATURE:
                                                MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                TOPOLOGY:
                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1825 Sharp Point Drive CITY: Fort Collins
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                 NAME/KEY:
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 LOCATION:
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100.0%; Pr
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RESULT 6 5213972-6/c ;Patent No. 5213972

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Query Match
Best Local Similarity
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US-09-005-051-16
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                                                                                                                                ; MOLECULE TYPE: US-09-005-051-17
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US-09-005-051-17
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                                               Query Match
Best Local Similarity
Matches 18; Conserv
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Patent No. 6291222
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APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
1002 ctccaaattcagaaatcc 1019
                                                                                                                                                                                                                                                                            FILING DATE: NO. 6291222ember: ATTORNBY/AGENT INFORMATION:
NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                      TELEPHONE: 9/0/-
TELEPHONE: 9/0/484-9505
TD NO:
                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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Pred. No.
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Pred. No.
                                                          Mismatches
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46;
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                                                                                     Length 1515;
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US-08-747-221B-60
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FILING DATE: 08-DEC-1989
SEQ ID NO:6:
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                           TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/747,2
FILING DATE: NO. 6063610ember 1
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MCCANDLISS, RUSSELL J.; ANDERSON, DAVID M. TITLE OF INVENTION: FERMENTATION PROCESS FOR THE PRODUCTION
                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid TITLE OF INVENTION: Molecules, Proteins and Uses Thereof NUMBER OF SEQUENCES: 66
                                                                                                                           FEATURE
                                                                                                                                                                          FEATURE:
                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1825 Sharp
CITY: Fort Collins
STATE: Colorado
                                                                                   NAME/KEY: Asx - Asn or LOCATION: 433
                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 80525
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E: Heska Corporation
1825 Sharp Point Drive
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1..1650
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No. 435
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100.0%; Pred. No.
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      Score 18;
Pred. No.
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47;
      DB 3;
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                    Length 1650;
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-747-221B-61
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                                                                                                                                                                                                                                                                                                                          Sequence 60, Application US/09005051 Patent No. 6291222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61, Application US/08747221B Patent No. 6063610
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                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPUTER:
COMPUTER: Windows 95
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
TINGER OF THE COMPUTER OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272 TELEPAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                         TITLE OF INVENTION: NCTITLE OF INVENTION: MCNUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1002 ctccaaattcagaaatcc 1019
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TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
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       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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Wisnewski, Nancy
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Carol Talkington Verser, Ph.D Heska Corporation
                                                                                                       Molecules, Proteins and 66
                                                                                                                                                                                 No. 6291222el Carboxylesterase Nucleic
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STREET: 1825 Sharp Point Drive CITY: Fort Collins

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Patent No. 6291222
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talvinger
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           APPLICANT: Silver, Gary W.

APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                              COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
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NAME/KEY:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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LOCATION:
          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                               COUNTRY:
                                                                                                                                                                                ADDRESSEE: Carol Talkington Verser, Ph.D ADDRESSEE: Heska Corporation
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STRANDEDNESS: single
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18; Conserv
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Pred. No.
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Best Local :
                                 INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:

CORRENT APPLICATION NUMBER: US/08/857,213
                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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SEQUENCE CHARACTERISTICS:
LENGTH: 1721 base pair
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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APPLICANT: Hawkins, Phillip R.
APPLICANT: Murry, Lynn E.
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NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
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APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                       FILING DATE:
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CITY: Palo Alto
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                                                                                                                                  36,749
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47;
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TOPOLOGY: line
IMMEDIATE SOURCE:

linear

single

FIBRNGT01

STRANDEDNESS:

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/139,937
FILING DATE: 20-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/979,156
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERY
NAME: CAMPBELL, CATHERY
NAME: CAMPBELL, CATHERY
                                                                                                                                                       Query Match
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Best Local :
                                                                                                                         Matches
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Patent No. 5821070
                                                                                                                                                                                                                                                                                                         TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                   2831 aaagaaccctctgaaaaa 2848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CELLULAR GENES ENCODING TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LEE, WEN-HWA
APPLICANT: SHAN, BEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4370 LA JOLLA VILLAGE DRIVE CITY: SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 atgaatttcataaaggac 53
                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 31
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIBRARY: FIBRA
CLONE: 148415
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ZIP: 92122
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les 18; Conserv
                                                                                                                                     Local
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                                                                                                                       l Similarity
18; Conserv
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                                                                                                                     0.6%; Score 18; llarity 100.0%; Pred. No Conservative 0; Mismat
                                                                                                                                                                                                                                              linear
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Pred. No.
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                                                                                                                       Mismatches
                                                                                                                                     . No.
                                                                                                                                     DB 1;
. 47;
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                                                                                                                                                       Length 1800;
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                                                                                                                                                                                                                                                                                                                                            sequence 13, Application US/08747221B Patent No. 6063610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application PC/TUS9311310
GENERAL INFORMATION:
APPLICANT: BOARD OF REGERTS OF THE UNIVERSITY OF TEXAS SYSTEM
TITLE OF INVENTION: CELLULAR GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
             COMPUTER READABLE FORM:
MEDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: CAMPBELL, CATHRYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                           APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 619-535-9001
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: CELLULAR GENES ENCODING TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 AAAGAACCCTCTGAAAAA 324
                                                                                                                        CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 19-NOV CLASSIFICATION:
                                                                                                         COUNTRY:
                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 31.
REFERENCE/DOCKET NUMBER:
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ZIP: 92122
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SOFTWARE:
                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                          80525
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                                                                                                                                                          IE: Carol Talkington Verser, Ph.D.
IE: Heska Corporation
1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                       USA
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WordPerfect for Windows, Version 7.0
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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19-NOV-1993
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                                                                                                                                                                                                                                                       No. 6063610el Carboxylesterase Nucleic Acid Molecules, Proteins and Uses Thereof
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100.0%; Pred. No. 47;
ive 0; Mismatches
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47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1800;
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CURRENT APPLICATION DATA:

ATTORNEY/AGENT INFORMATION: NAME: Verser, Carol Talk

CLASSIFICATION:

FILING DATE: APPLICATION NUMBER:

No.

6063610ember 12, 1996

US/08/747,221B

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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                             APPLICATION UNBER: US/08/747,22:
APPLICATION UNBER: US/08/747,22:
FILING DATE: NO. 6063610ember 12.
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Silver,
                                  TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1002 ctccaaattcagaaatcc 1019
SEQUENCE CHARACTERISTICS:
LENGTH: 1982 nucleotic
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOTTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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LOCATION:
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LOCATION:
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REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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Colorado
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Pred. No.
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1002 ctccaaattcagaaatcc 1019

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                                                                              US-09-005-051-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 18; Conserv
Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09005051 Patent No. 6291222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Silver, (
APPLICANT: Wisnewsk
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1618 CTCCAAATTCAGAAATCC 1635
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1002 ctccaaattcagaaatcc 1019
                                                                                                                              FEATURE
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1982 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                          FEATURE
                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC
                                                                                                                                                                                                                                                                                                                                                                 NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1825 Sharp Point Drive CITY: Fort Collins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wisnewski,
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Silver, Gary W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                               Asx = Asn or Asp
300
                                                                                                                                                                                                                                                                                                                    970/493-7272
              0.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i, Nancy
No. 6291222el Carboxylesterase Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%;
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Pred. No.
                  Score 18;
Pred. No.
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
                  DB 4;
47;
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                               Length 1982;
 Indels
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Gaps
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RESULT 17 US-09-005-051-15

Sequence 1 Patent No.

15, Application US/09005051 o. 6291222

GENERAL INFORMATION:

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365 CTCCAAATTCAGAAATCC 348

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RESULT 18
US-08-747-221B-57/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.6%; Score 18; Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 970/40+ ... 15
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
TENGTH: 1982 nucleotides
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-005-051-15
                                                                             APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nancy TITLE OF INVENTION: NO. 606 TITLE OF INVENTION: MOLECUL NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1002 ctccaaattcagaaatcc 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/747,221 FILING DATE: NO. 6291222ember 12, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOTTWARE: Wordberfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Wisnewski, Nancy
APPLICANT: Wisnewski, Nancy
APPLICANT: Wisnewski, Nancy
APPLICANT: Misnewski, Misnewski, Nancy
APPLICANT: Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski, Misnewski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1
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CITY: Fort Collins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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        ADDRESSEE:
                                           ADDRESSEE:
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Carol Talkington Verser, Ph.D Heska Corporation
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                                                                                                                                                               Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                          i, Nancy
No. 6063610el Carboxylesterase Nucleic Acid
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. 47;
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RESULT 19
US-08-747-221B-59
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                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 59, Application US/08/147221B Patent No. 6063610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nano
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordberfect for Windows, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B FILING DATE: NO. 6063610ember 12, 15 CLASSIFICATION: 435
ATTORNEY/ACTION: 435
                SOFTWARE: WordPerfect for Windows, Version 7.0 CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1002 ctccaaattcagaaatcc 1019
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527 CTCCAAATTCAGAAATCC 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                  STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95
FILING DATE: N
CLASSIFICATION:
                                                                                                                                                       COUNTRY: U
ZIP: 80525
                                                                                                                                                                                                                                         ADDRESSEE: Heska Corporation

ADDRESSEE: Heska Corporation
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nes 18; Conserv
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 970/483-72
TELEFAX: 970/484-9505
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30..1682
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                                                                                                                   Floppy disk
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 435
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                                                                                                                                                                                                                                                                                                                 No. 6063610el Carboxylesterase Nucleic Acid Molecules, Proteins and Uses Thereof
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                                                                                                                                                                                                                                                                                                                                                  Nancy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2144;
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ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol REGISTRATION NUMBER:

Carol Talkington

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RESULT 20
US-09-005-051-57/c
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/747,221
APPLICATION UNMBER: 08/222ember 12, 19
FILING DATE: No. 6291222ember 12, 19
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
                                                                                                                                                        TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 57:
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                                                                                                                                                                                                REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2144 nucleotides
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REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                       MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
 LOCATION:
                  NAME/KEY:
                                                                       TOPOLOGY: linear
                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                        2144 nucleotides
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CDS
30..1682
                                                      CDNA
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Pred. No.
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US-09-005-051-59
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; LOCATION:
US-09-005-051-57
                                                                                                                         US-09-005-051-59
                                                    Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/09005051 Patent No. 6291222
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Best Local Similarity
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                                                                                                                                                                                                                  TELEPHONE: 970/493-72:
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2144 nucleotid
                                                                                                                                                                                                                                                                                                                FILING DATE: No. 6291222ember 12, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                       NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1825 Sharp Point Drive CITY: Fort Collins
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VENTION: No. 6291222el Carboxylesterase Nucleic
VENTION: Molecules, Proteins and Uses Thereof
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silver, Gary W.
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                                                                                                                                                                single
                                                              100.0%;
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                                                                   0.6%; Score 18; DB 4; 100.0%; Pred. No. 47;
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Pred. No.
                                                      Mismatches
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                                                      Indels
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RESULT 22 US-09-192-104-1

Sequence 1, Application US/09192104B Patent No. 6184020

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; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Sphingomonas
US-09-543-446-1
                                                                                                                                                                                     TITLE OF INVENTION: Polypeptides Having Aminopeptidase
TITLE OF INVENTION: Activity And Nucleic Acids Encoding San
FILE REPERENCE: 5379.210-US
CURRENT APPLICATION NUMBER: US/09/543,446
CURRENT FILING DATE: 2000-04-05
EARLIER APPLICATION NUMBER: 60/069719
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 1465/97
EARLIER APPLICATION NUMBER: 1465/97
EARLIER APPLICATION NUMBER: 1998-00670
EARLIER FILING DATE: 1998-05-15
EARLIER FILING DATE: 1998-05-15
EARLIER FILING DATE: 1998-05-15
EARLIER APPLICATION NUMBER: 09/192,104
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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEG ID NO 1
; LENGTH: 3000
; TYPE: DNA
; ORGANISM: Sphingomonas
US-09-192-104-1
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APPLICANT: Tony Byun
APPLICANT: Alan V. Klotz
APPLICANT: Alan Sloma
APPLICANT: Maria Tang
APPLICANT: Mikio Fujii
APPLICANT: Chigusa Marumoto
APPLICANT: Lene Venke Kofod
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%;
Best Local Similarity 100.0%;
Matches 18; Conservative
                                                                                            SOFTWARE: FastSEQ
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Alexander Blinkovsky
APPLICANT: Tony Byun
APPLICANT: Alan V. Klotz
APPLICANT: Alan Sloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/192,104B
CURRENT FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/069719
EARLIER FILING DATE: 1997-12-16
EARLIER APPLICATION NUMBER: 1455/97
EARLIER FILING DATE: 1997-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Polypeptides Having Aminopeptidase TITLE OF INVENTION: Activity And Nucleic Acids Encoding FILE REFERENCE: 5379.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: PA 1998 00670 EARLIER FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Maria Tang
APPLICANT: Mikio Fujii
                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                    EARLIER FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chigusa Marumoto
APPLICANT: Lene Venke Kofod
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                                                                                                                  for Windows Version 4.0
                                                                                                                                                                    1998-11-13
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Pred. No.
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47;
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US-09-037-990B-27
Sequence 27, Application US/09037990B; Patent No. 6248519
GENERAL INFORMATION:
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                                                                                                                                                                                                                                Query Match
Best Local:
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Best Local
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/322-507
TELEFAX: 650/854-0875
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002
FILING DATE: 17-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                        1743 CCCTTGGTGAAGATATTG 1726
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/322-5070
TELEPHONE: 650/854-0875
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rine, Jasper D.
APPLICANT: Hampton, Randol
TITLE OF INVENTION: GENES
TITLE OF INVENTION: CHOLES
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1911 gctggtgtggctggaagc 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2127 gctggtgtggctggaagc 2144
                                                                                                                                                                       391 cccttggtgaagatattg 408
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CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/699, 103B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
APPLICANT: ENGEL, Stacia R.
DESCENZO, Richard A.
MORENZONI, Richard A.
                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                  Similarity 100.
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                        4982 base pairs
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                                                                                                                                                                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                                                                                                         single
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100.0%; Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P.C.
Suite
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47;
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                                                                                                                                                                                                                                                Length 4982;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 27: US-09-037-990B-27
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                              Sequence 171, Applicat Patent No. 6225054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1152 aaaaacaaacacaaaca 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209 AAAAACAAACACAAACA 225
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
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APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                      APPLICANT: Frudakis, Tony N. Smith, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/037,990B FILING DATE: 11-Mar-1999 CLASSIFICATION: <Unknown>
                                                                              ZIP: 98104-7092
                                                                                              STATE: Washington COUNTRY: USA
                                                                                                                                     CITY: Seattle
                                                                                                                                                 ADDRESSEE: Seed IP Law Group
Soite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sharp, Jeffrey S. REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRELAN, NAMEY A.

OF INVENTION: DETECTION OF FERMENTATION-RELATED
                                                                                                                                                                                                                                                                                                                                                                    Application US/08991789A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                          Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 17;
100.0%; Pred. No.
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. 1.4e+02;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09037990B Patent No. 6248519 GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/037,990B
FILING DATE: 11-Mar-199
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
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REGISTRATION NUMBER: 33,32
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                     TELEPAN: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 383 base pairs TYPE: nucleic acid
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                                                                                                                                       NAME: Sharp, Jeffrey S. REGISTRATION NUMBER: 31,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Illinois
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCENZO, Richard A. MORENZONI, Richard A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRELAN, Nancy A.
VENTION: DETECTION OF FERMENTATION-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marshall, O'Toole, Gerstein, Murray & Borun
30 Sears Tower, 233 South Wacker Drive
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682-6031
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; Pred. No.
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. 1.4e+02;
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-037-990B-8
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                                                                                     US-08-998-416-818
   Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                 TOPOLOGY: line MOLECULE TYPE: I ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 685 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
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APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                       ORGANISM:
                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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     Conservative
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VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wendland, Jurgen
Knechtle, Philipp
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Steiner, Sabine
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                                                                                                                                      DNA (genomic)
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                   0.5%;
                                                                                                                                                                                                                                                                                           38,241
ER: PF/5-30306/A/CGC1976
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Score 17; DB 4; Le
; Pred. No. 1.4e+02;
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Pred. No.
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                                 Length 685;
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     Indels
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LENGTH: 1536
TYPE: DNA
ORGANISM: Homo sapiens
US-09-318-443-5
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US-09-318-443-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 183
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Best Local :
                                          APPLICATION NUMBER: US/08/743,637B FILING DATE: 04-NOV-1996 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Weinstein, Daniel C.
TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIII,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-211 N
CURRENT APPLICATION NUMBER: US/09/318,443
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 12
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CITY: MILWAUKEE
STATE: WISCONSIN
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                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                  COUNTRY:
              REGISTRATION NUMBER:
                             NAME: BAKER, Jean C.
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BERGERON, Michel G.
PICARD, Francois J.
OUELLETTE, Marc
ROY, Paul H.
                                                                                                                                                                                                                                                                                                                                                         411 EAST WISCONSIN AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08743637B
                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                          IBM PC compatible PC-DOS/MS-DOS
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 NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                         PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOCENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ... 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-SPECIFIC AND UNIVERSAL DNA
                                                                                                                                                      US/08/743,637B
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850586.90012
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; LENGTH: 1682
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-443-7
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                                                                                                                                                                                                                                                                                                          US-09-178-252-26
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09318443 Patent No. 6197947 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Sequence 26, Application US/09178252 Patent No. 6218188
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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SEQ ID NO
                           APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 05/05/215
EARLIER APPLICATION NUMBER: 60/065,215
EARLIER APPLICATION NUMBER: 60/065,215
EARLIER FILING DATE: 1997-11-12
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Weinstein, Daniel C.
TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-211 N
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INFORMATION FOR SEQ ID NO:
                  SOFTWARE: PatentIn Ver.
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MOLECULE TYPE: [
ORIGINAL SOURCE:
ORGANISM: Klek
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100.0%; Pr
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100.0%; Pred. No.
Live 0; Mismatc
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-960-780-10
INDIVIDUAL ISOLATE: US-08-960-780-10
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Best Local S
Matches 17
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                                                                                                                    TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-CCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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                               ORIGINAL SOURCE:
                                         MOLECULE TYPE:
                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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nes 17; Conser
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                                                              TOPOLOGY:
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Gainesville
                                                                          STRANDEDNESS:
                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                NAME: Saliwanchik, David R
                                                                                                       LENGTH: 2035 base pairs
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                                                                                         nucleic acid
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Stamp, Lisa
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Dullum, Charles Joseph
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                                                            linear
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                                              DNA (genomic)
                                                                          single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 6204435el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
134
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               158C2-pt1
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; Pred. No.
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                                                                                                                   ; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: 158C2-pt1
US-09-073-898-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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2620 aagatggaaatgaagct 2636
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PRIOR APPLICATION NUMBER: US 60/029,848
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APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
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                    0.5%; Score 17;
Local Similarity 100.0%; Pred. No.
les 17; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                    NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/073,898 FILING DATE:
                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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ZIP: 32606-6669
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Dullum, Charles Joseph
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                                    Mismatches
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hes 0;
                                                   1.4e+02;
                                                                 Length 2035;
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US-09-115-446-1
US-09-115-446-5
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                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Applic
Patent No. 6165719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: hKCA3/KCNN3 SMALL CONDUCTANCE CALCIUM TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOSTIC TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET FILE REFERENCE: 07306/014001
CURRENT APPLICATION NUMBER: US/09/115,446
CURRENT FILING DATE: 1998-07-14
EARLIER APPLICATION NUMBER: 60/052,556
EARLIER FILING DATE: 1997-07-15
                                                                                                                                                                                                                                                                              APPLICANT: Fantino, Emmanuelle
APPLICANT: Kalman, Katarin
TITLE OF INVENTION: hKCA3/KCNN3 SMALL CONDUCTANCE CALCIUM
TITLE OF INVENTION: ACTIVATED POTASSIUM CHANNEL: A DIAGNOS
TITLE OF INVENTION: MARKER AND THERAPEUTIC TARGET
FILE REFERENCE: 0/306/014001
                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/052,556 EARLIER FILING DATE: 1997-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chandy, George APPLICANT: Gargus, Jay J. APPLICANT: Gutman, George
                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/070,741 EARLIER FILING DATE: 1998-01-08
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/115,446
CURRENT FILING DATE: 1998-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gargus, Jay J. APPLICANT: Gutman, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chandy, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fantino, Emmanu APPLICANT: Kalman, Katarin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/070,741
                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ
                                                            LENGTH: 2526
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LOCATION: (28)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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100.0%; Pred. No.
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US-08-095-737-1/c
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NAME: ISTRAELSEN, Ned A
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 1:
                           Sequence 1, Application US/08480145
Patent No. 5717067
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Best Local Similarity
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   GENERAL INFORMATION:
APPLICANT: Difior
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                                                                                                                              2811 attttaggtgcattttt 2827
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APPLICATION NUMBER: US
FILING DATE: 19930722
                                                                                                                   4070 ATTTTAGGTGCATTTTT 4054
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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mes 17; Conservative
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STRANDEDNESS: doub
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California
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DiFiore, Pier P
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Pred. No.
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US-08-477-389-1/c
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Matches
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                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                         APPLICANT: DiFiore, Pier P
APPLICANV: Fazioli, Frances
TITLE OF INVENTION: A Subst
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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nes 17; Conservative
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
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                                                COUNTRY:
                                                                                             STREET:
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                                                                California
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A Substrate for the Epidermal Growth
Factor Receptor Kinase
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A Substrate for
Factor Receptor
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Sixteenth Floor
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Kinase
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE:

PatentIn Release #1.0, Version #1.25

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US-08-477-389-1
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US-08-559-303B-72
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Patent NO. 5824501

GENERAL INFORMATION:
APPLICANT: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA
APPLICANT: GRODEN
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMITITLE OF INVENTION: OF BLOOM'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
               NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 63475/65
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/559,:
FILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
AMSTER, ROTHSTEIN & EBENSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4070 ATTTTAGGTGCATTTTT 4054
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                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Israelsen, Ned A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                      CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/0 FILING DATE: 22-JUL-1993
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                                                                                                                                                                                                                                                       ZIP: 10016
                                                                                                                                                                                                                                                                                                                     STREET:
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07-JUN-1995
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286-0854 or 286-0082
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                                                                                                                                   US/08/559,303B
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US-09-175-828-72
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Best Local Similarity
Matches 17; Conserv
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INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTU. 4427
                                                                                                                                                                                                                                                                     TELEFAX: (212) 286-0854
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL: 1
ANTI-SENSE: NO
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APPLICATION NUMBER: US/09/175,828
                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/559,:
ATILING DATE: NOVEMBER 15, 1995
ATTORNEY/AGENT INFORMATION:
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AMSTER, ROTHSTEIN & EBENSTEIN
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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HYPOTHETICAL:
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                               DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: ELIZABETH A. BOGOSIAN REGISTRATION NUMBER: 39,911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
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CITY: NEW YORK
STATE: NEW YORK
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LOCATION:
                                                                                                  TOPOLOGY:
                                                                                                                               STRANDEDNESS:
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100.0%; Pr
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39,911
~~R: 63475/65
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; Pred. No. 1.4e+;
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ANTI-SENSE:

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; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: MYCODOCTETIUM tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Best Local Similarity
Thes 17; Conserve
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: FILEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/08137117D Patent No. 5795965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                NUMBER OF SEQUENCES: 158
CORRESPONDENCE ADDRESSE: Poley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                               APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
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                                                  COUNTRY:
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                                                                                   Washington
                                                                  D.C.
                                                    USA
                                                                                                                                                                                                             BENDIG, Mary
JONES, Steven
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100.0%; Pred. No.
Pative 0; Mismath
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Pred. No.
                                                                                                    Suite 500
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US-08-436-717-48/c
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                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/436,717
                                                                                                                                               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/137,117D FILING DATE: 20-DEC-1993
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     APPLICANT: SALDANHA, JOSE
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY
TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
NUMBER OF SEQUENCES: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 3-95476
FILING DATE: 25-APR-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 25,258
REGISTRATION NUMBER: 53466/126/AAOK
                                                    FILING DATE:
                                                                                                                                                                                COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                      STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                   D.C
                                                                                                                                                                                                                                                  3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                   BENDIG, Mary
JONES, Steven
                                                                                                                                                                                                                                                                                                                                                    SALDANHA,
                                                                                                                                                                                                                                                                                                                                                                                                        SATO, Koh
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Conservative
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19-FEB-1992
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   US/08/137,117
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Pred. No.
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PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

24-APR-1992

JP 4-32084

20-DEC-1993 JMBER: WO PCT/JP92/00544

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 153, Application US/08943731
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                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET,
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES: 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
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ATTORNEY/AGENT INFORMATION:
NAME: WECKER, Harold C.
REGISTRATION NUMBER: 25,258
BEFERENCE DOCKET NUMBER: 53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                  PRIOR APPLICATION DATA:
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TELEFAX: 904136
TEX: 904136
                                                                                                                                                                                                                                                                                            STREET:
                                                 APPLICATION NUMBER: US/08/943,731 FILING DATE: 03-OCT-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-7086
                                                                                                                                                                                                                                                             STATE:
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APPLICATION NUMBER: US 08/212,322 FILING DATE: 14-MAR-1994
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SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
LARISA W.
                                                                                                                                                                                                                                                                                                                                                                                                                          ALA-KOKKO, LEENA, et al
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EARLY, JAMES
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4.1e+02
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; MOLECULE TYPE: US-08-479-577-1
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GENERAL INFORMATION:
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                                                                                             TELEFAX: (203)268-1951 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (203)268-1951
                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Milton Zaitlin, and Peter Palukaitis TITLE OF INVENTION: Induction Of Resistance To TITLE OF INVENTION: Viral Diseases In Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
TELEFAX: 215-567-2991
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APPLICATION NUMBER:
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                               STRANDEDNESS:
TOPOLOGY: lir
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OPERATING SYSTEM:
                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                            NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Microsoft Word 4.0
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Trumbull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
                                                                                LENGTH:
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16; Conserv
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                                                               nucleic acid
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                                                                              132 base pairs
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03-DEC-1991
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100.0%; Pred. No.
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25 Skytop Drive

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RESULT 48
PCT-US93-05331-5/c
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                                                                             Sequence 5, Application PC/TUS9305331
GENERAL INFORMATION:
APPLICANT: Cornell Research Found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08756977 Patent No. 5945581
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTĒRISTICS:
LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                              2541 gcagtgaaaatcctag 2556
|||||||||||||||||
| 100 GCAGTGAAAATCCTAG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,977
FILING DATE: 26-NOV-1996
CLASSIFICATION: 800
                                              APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Induction Of Resistance To
TITLE OF INVENTION: Virus Diseases By Transformation Of Plants With A Replicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zaitlin, Milton
APPLICANT: Palukaitlis, Peter
TITLE OF INVENTION: INDUCTION OF RESISTANCE TO VIRAL
TITLE OF INVENTION: DISEASES IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2541 gcagtgaaaatcctag 2556
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
               NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Goldman, Michael REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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   ADDRESSEE:
                                                                                                                                                                                                                                                                 16;
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
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                                                                                                                                                                                                                                                                 Conservative
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Yahwak & Associates
                                                                                                                                                                                                                                                                                                                                                                RNA (genomic)
                                                                                                                                                                                                                                                                                 100.0%;
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htive 0;
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30,727
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                 Mismatches
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4.1e+02;
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                                                                                                                                                                                                                                                                                 4.1e+02;
                                                                                                                                                                                                                                                                                                Length 132;
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
PCT-US93-05331-5
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Patent No. (
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Best Local Similarity
Matches 16; Conserv
            COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/621,018B
FILING DATE: MARCh 22, 1996
PRIOR APPLICATION NUMBER: 08/409,373
APPLICATION NUMBER: 08/409,373
APPLICATION NUMBER: 39,132
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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LENGTH: 132 base pairs
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Trumbull
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CITY: Palo Alto
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                              MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                  94304
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Seilhamer, Jeffrey J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (203)268-1951
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Stuart, Susan G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 100.0%; | Conservative 0;
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PF-0029-1 CIP
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RESULT 50
US-08-171-385-26
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                                                               TOPOLOGY: 0S-08-171-385-26
Query Match
Best Local Similarity
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Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Watches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/08171385 Patent No. 5527884 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEORMATION FOR SEQ ID NO:
                                                                                                                                                                                                   NAME: Fraser, Janis K.
REGISTION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 054
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS (Version 5 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mary E. Russell APPLICANT: Ulrike Utans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
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                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PS/2 Model 50z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0)
                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                                                        TELEFAX: (617) 542-8906
TELEX: 200154
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                                                                                                                          ENGTH:
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                                                                                                                             300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 Franklin Street
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   Score 16;
Pred. No.
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   4.2e+02;
                 DB 1;
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                 Length 300;
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                                                                                                                                                Patent No.
                                                                                                                                                  Sequence 40, Application US/08916576B Patent No. 6171816
                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 617/542-50:
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                          APPLICANT: YU, GUO-LIANG
APPLICANT: DILLON, PATRICK J.
APPLICANT: EBNER, REINHARD
APPLICANT: ENDRESS, GREGORY A.
TITLE OF INVENTION: NOVEL HUMAN GROWTH FACTORS
                                                                                                                                                                                                                                                                    1995 aactggaagcaggaat 2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 300 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 21-DEC-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Russell, Mary E. APPLICANT: Utans, Ulrike
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                                                                                                                                                                                                                                                   282 AACTGGAAGCAGGAAT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 300 base pair TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Fraser, Janis K REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish .... Street
 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                   16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6, Application US/08361441B 6077948
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                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
                                   45
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                                                                                                                                                                                                                                                                                                                                 Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                    4.2e+02;
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                                                                                                                                                                                                                                                                                                                                               Length 300;
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                                                                                                                                                                                                                                                                                                                  0;
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COUNTRY:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 78, Application US/08991789A Patent No. 6225054
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 4 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
EILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1820 atttgacttctttgaa 1835
|||||||||||||||||||
| 108 ATTTGACTTCTTTGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
                                                    CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                           STATE: Washington
                                                                                                                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Seed IP Law Group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0,
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Reed, Steven G.
                                                                                                                                                                                                                                                                                                 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y 100.0%; Score 16;
rvative 0; Mismar-
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hes 0;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 248:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO: 78:
2557 ctcagaatcttcacaa 2572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2557 ctcagaatcttcacaa 2572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 0.5%; Sy Local Similarity 100.0%; I hes 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
ADDRESSEE: ADDRESSEE: Seed IP Law Group
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: POLTET, Jane E. R.
REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 78:
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                                                                                                                                                                        LENGTH: 355 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 701 F:
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/991,789A FILING DATE: 11-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 355 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08991789A
                                                    Conservative
                                                                   0.5%;
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                                                  Score 16; DB 4; L; Pred. No. 4.2e+02; 0; Mismatches 0;
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149 CTCAGAATCTTCACAA 164

RESULT 55 US-08-470-179-100

Sequence 100, Appl Patent No. 5645994

Application US/08470179

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US-08-943-731-127
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Best Local Similarity 100.
Thes 16; Conservative
                                                                                                                                                  Sequence 127, Application US/08943731 Patent No. 6265157
                                                                                                                                                                                                                                                                                                                                                                                -08-470-179-100
                                                                                                                   GENERAL INFORMATION: APPLICANT: PROCKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 801-531-9168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "gyrA gene segment"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 801-532-1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Huang Ph.D, Wai Mun
TITLE OF INVENTION: Method and
TITLE OF INVENTION: Identifical
NUMBER OF SEQUENCES: 207
                          APPLICANT
                                                                                     APPLICANT:
                                                                                                        APPLICANT:
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                                            APPLICANT:
                                                           APPLICANT:
                                                                        APPLICANT:
                                                                                                                                                                                                                                             107
PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Swedgert Ph.D, Susan E. REGISTRATION NUMBER: 36,289
REGISTRATION NUMBER: 2601
                                                                                                                                                                                                                                                         14 tgggaagctttcatcc 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/470,179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Trask, Britt and Rossa
P.O. Box 2550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                    SPOTILA,
           COLIGE, ALAIN EARLY, JAMES
                                                        SEREDA, LARISA
LARSON, ANDREA W.
                                            PACK,
                                                                                      DELTAS, CONSTANTINOS D.
                                                                                                                   PROCKOP, DARWIN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                          MICHAEL
                                                                                                                                                                                                                                                                                                                   0.5%;
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                                                                                                    LORETTA D
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                    Score 16; Pred. No.
                                                                                                                                                                                                                                                                                                      Mismatches
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Matches
                                                                                                                                                                                                                                                Sequence 14, Application US/08899786 Patent No. 6001572
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                STREET: BALL
STREET: Colorado
                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                               APPLICANT: Toothman, Penelope TITLE OF INVENTION: Method of NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                1979 tgtatctttgttcttc 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 434 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-MAR-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UPPLICATION DATE: 03-OCT-1 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-DEC-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                196 TGTATCTTTGTTCTTC 211
                                                             COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: ....STRANDEDNESS: qui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: DOYLE LEARY Ph.D., KATHRYN REGISTRATION NUMBER: 36,317 REFERENCE/DOCKET NUMBER: 9598-27
COMPUTER: IBM pc compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0: FILING DATE: 14-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19103-7086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: PANITCH SCHWARZE JACOBS & NADEL, P.C. ONE COMMERCE SQUARE, 2005 MARKET STREET,
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALA-KOKKO,
                                                                                                                             Swanson & Bratschun, L.L.C.
00 E. Prentice Avenue, Suite 200
                              Diskette, 3 1/2 diskette, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     umber: US/08/943,731
03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
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COMPOSITIONS AND METHODS FOR DETECTING

ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                           Method of Identifying Aloe Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 434;
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SOFTWARE: Wordperfect 8.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER:

US/08/899,786

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RESULT 58
US-08-899-786-16/c
; Sequence 16, Application US/08899786
natent No. 6001572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1
MOLECULE TYPE:
5-08-899-786-14
                                                              TELEFAX: (303) 793-34 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (303) 793-34
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
              SEQUENCE CHARACTERISTICS:
LENGTH: 562 base pairs
TYPE: nucleic acid
                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
0/022,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 gatttggctcaggatt 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 GATTTGGCTCAGGATT 83
                                                                                                                                                                                     APPLICATION NUMBER: 60/02: FILING DATE: 26-JULY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Englewood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/02 FILING DATE: 26-JULY-1996
                                                                                                                         REFERENCE/DOCKET NUMBER: UNI.07
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                               80111
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                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (303) 793-3333
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                                                                                                                                                                                                                                                                                                                                              3 1/2 diskette,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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Best Local Similarity
Thes 16; Conserve
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GENERAL INFORMATION:
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                                                                                                    TELEFAX: 703-816-4100 (INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
ANTI-SENSE: NO ORIGINAL SOURCE:
               TOPOLOGINAL: N
                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/005,840
FILING DATE: 23-OCT-1955
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/96GB/02588
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/042,655
FILING DATE: 02-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SPURR, NIGEL K
APPLICANT: GRAY, IAN C
APPLICANT: STEWART, LORNA M
TITLE OF INVENTION: DIAGNOSIS OF SUSCEPTIF
TITLE OF INVENTION: AND TREATMENT THEREOF
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                             REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-DEC-
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                              STRANDEDNESS:
                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                               LENGTH:
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                                                                              nucleic acid
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                                                                                                 573 base pairs
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1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                  linear
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                                 NO
                                                                                                                                                                                                                                                                                                                                                          NUMBER: US 60/033,147
13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                           36,663
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. 4.2e+02;
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CORRESPONDENCE ADDRESS:

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                                                                                                                                  RESULT 61
US-08-906-156A-19/c
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                                                                                                     Sequence 19, Application US/08906156A Patent No. 6287854
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
             APPLICANT: SPURR, NIGEL K
APPLICANT: GRAY, IAN C
APPLICANT: STEWART, LORNA M
TITLE OF INVENTION: DIAGNOSI
TITLE OF INVENTION: AND TREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: UN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 574 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 8.0
CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 tcattcacatgatttt 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8400 E. Prentice Avenue,
                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                          single
DIAGNOSIS OF SUSCEPTIBILITY TO CANCER AND TREATMENT THEREOF 94
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Pred. No. 4.2e+02;
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RESULT 62
US-09-385-982-233
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                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O.,
                                                                                                                                                                                                                                Patent No. 626233
                                                                                                                                                                                                                                                    Sequence 233,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                          TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDNA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
                                                        EARLIER APPLICATION NUMBER: 09/328,111 EARLIER FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 590 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/033,147
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,840
FILING DATE: 23-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/042,655 FILING DATE: 02-APR-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 40 PCT/96GB/02588
FILING DATE: 2-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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100.0%; Pred. No.
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4.2e+02;
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EARLIER FILING DATE: 1998-08-31

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RESULT 64
US-09-385-982-101/c
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                                                                                            В
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; LCCATION: (1)...(603)
; OTHER INFORMATION: n = A,T,C
US-09-385-982-233
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Sequence 101, Application US/09385982 Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                  EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
[SEQ ID NO 205
LENGTH: 607
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 233
LENGTH: 603
                                                                                                                                                                  Query Match
Best Local 9
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Best Local Similarity
                                                                                                                                                     Matches
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APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT SPELICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burgess, Christopher C. Bushnell, Steven E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Astle, Jon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steinmann, Kathleen
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100.0%;
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Pred. No.
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Pred. No.
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                                                                                                                                                                              Length 607;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/08468347 Patent No. 5783421
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Best Local Similarity
Matches 16; Conserv
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APPLICANT: ENDEGE, WILSON O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS: II FILE REFERENCE: CCDNA-260XX
                                  ATTORNEY_AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/385,982 CURRENT FILING DATE: 1999-08-30
TELEPHONE: 212-977-95
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO:
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EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
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LOCATION: (1)...(625)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 625
                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Zeelon, Elisha P
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL P
TITLE OF INVENTION: INHIBIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
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NOVEL POLYPEPTIDE HAVING FACTOR
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Pred. No.
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4.2e+02;
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

LENGTH:

697 base pairs

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; MOLECULE TYPE: DNA (genom.; HYPOTHETICAL: NO; ANTI-SENSE: NO; FRAGMENT TYPE: N-terminal US-08-468-347-25
                                                                                           US-08-467-389-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-467-389-25/c
Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEPAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/225,44
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317
                                                                                                        HYPOTHETICAL: NAME OF ANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2940 ttttttgactttagta 2955
                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  678 TTTTTTGACTTTAGTA 663
                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York ZIP: 10112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                        697 base pairs
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        Conservative
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                                                                                                                                                                           linear
                                                                                                                                            NO
                                                                                                         N-terminal
                                                                                                                                                        DNA (genomic)
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                    0.5%; Score 16; DB 1; L
100.0%; Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOVEL POLYPEPTIDE HAVING FACTOR Xa
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100.0%; Pred. No.
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   0;
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        Mismatches
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4.2e+02;
      0;
                                       Length 697;
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      Indels
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      0,
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      Gaps
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      0;
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; MOLECULE TYPE: D
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N
US-08-779-379-25
                                                                                                             RESULT 68
US-08-469-219-25/c
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US-08-779-379-25/c
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                                                                             Sequence 25, Application US/08469219 Patent No. 5863534
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                                                                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO:
APPLICANT: Zeelon, I
APPLICANT: Werber, I
APPLICANT: Levanon,
TITLE OF INVENTION:
                                                                                                                                                                                             2940 ttttttgactttagta 2955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zeelon, Elisha P.
APPLICANT: Werber, Moshe M.
APPLICANT: Levanon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR
TITLE OF INVENTION: INHIBITORY ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 697 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212-977-9550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                              678 TTTTTTGACTTTAGTA 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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STATE: New Yor
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                                                                                                                                                                                                                                             16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 Rockefeller Plaza
                Levanon,
                               Werber, Moshe M.
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                        N-terminal
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                                                 Elisha P.
                                                                                                                                                                                                                                                          0.5%;
              Avigdor
NOVEL POLYPEPTIDE HAVING FACTOR Xa
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                                                                                                                                                                                                                                           0;
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TITLE OF INVENTION: NUMBER OF SEQUENCES:

INHIBITORY ACTIVITY 25

CORRESPONDENCE ADDRESS

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US-09-228-152-25
                                                                      CURRENT APPLICATION NUMBER: US/09/228,152
CURRENT FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
LENGTH: 697
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                              Sequence 25, Appl
Patent No. 621134
                                                                                                                                                                            APPLICANT: Levamon, Avigdor
TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR XA
FILE REFERENCE: 43020aya
                                                                                                                                                                                                                             APPLICANT: Zeelon, Elisha P. APPLICANT: Werber, Moshe M.
                                                                                                                                                                                                                                                                                                              -09-228-152-25/c
           OTHER INFORMATION: Description of Artificial Sequence: DNA sequence OTHER INFORMATION: of cDNA clone pSP65-XaI-13.
                                           FEATURE:
                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%;
ses 16; Conservative (
                                                                                                                                                                                                                                                                                            Application US/09228152
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                                                                                                      ; NAME/KEY:
; LOCATION:
US-08-916-576B-5
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                                                  Query Match
Best Local
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Best Local Similarity
                                       Matches
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                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1820 atttgacttctttgaa 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2940 ttttttgactttagta 2955
                                                                                                                                                                                                                                                                                                                                                             NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14!
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION UNDAFA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EBNER, F
APPLICANT: ENDRESS,
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                               FEATURE:
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                 Local
                                                                                                                                                           LOCATION:
                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               LENGTH:
                                       16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WASHINGTON
                                                                                                                                                                                                                                                                              nucleic acid
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VENTION: NOVEL HUMAN GROWTH FACTORS
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DILLON, PATRICK J.
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49..546
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49..117
                                                                                                                                                          mat_peptide
118..546
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                                                                                                                                                                                                                                                                   double
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                                                 0.5%;
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                                                  Score 16;
Pred. No.
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Pred. No.
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                                       Mismatches
                                 DB 4; LC.
3. 4.2e+02;
0;
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4.2e+02;
thes 0;
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                                     0,:
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TELEFAX: 212-664-0525 INFORMATION FOR SEQ ID NO:

25:

TELEPHONE: 212-664-0525

212-977-9550

TELECOMMUNICATION INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 08-APR-1994

08/225,442

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS

APPLICATION NUMBER: US/08/469,219 FILING DATE:

COMPUTER READABLE FORM:

COMPUTER:

MEDIUM TYPE:

STATE: NC. 10112

New York

STREET: ADDRESSEE:

E: Cooper & Dunham 30 Rockefeller Plaza

New York

SEQUENCE CHARACTERISTICS: LENGTH: 697 base pairs TYPE: nucleic acid

TYPE: nucleic STRANDEDNESS:

MOLECULE TYPE:

TOPOLOGY:

linear

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DNA (genomic) single

RESULT 71 US-08-152-485-3

Sequence 3, Application US/08152485 Patent No. 5539094

GENERAL INFORMATION:

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RESULT 72
US-08-463-089-3
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Best Local Similarity 100.0%;
Matches 16; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: FOR PC-DOS/MS-DOS
COMPUTER: FOR PC-DOS/MS-DOS
COMPUTER: FOR PC-DOS/MS-DOS
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COMPUTER: FOR PC-DOS/MS-DO
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152/485
FILING DATE: 10-NOV-1993
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Bcl-2-associated proteins NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Takayama, Shinichi APPLICANT: Sato, Takaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: p-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
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APPLICANT: Takayama, Shinichi
APPLICANT: Sato, Takaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                CITY: San Diego
STATE: California
                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                             92122
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                                                                                                                                                                 USA
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; Pred. No. 4.2e+
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hes 0;
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RESULT 73
US-08-461-360A-3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Takayama, Shinichi
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Bcl-2-asso
                                                                            TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             SOFTWARE: PatentIn Relea
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/O
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
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                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P:
TELECOMMUNICATION INFORMATION:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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LENGTH: 733 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 GTTGAAACATTTGGAG 244
                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 4370 La Jo
CITY: San Diego
STATE: California
             TOPOLOGY:
                           STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                              LENGTH:
                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                             nucleic acid
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                                                              733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4370 La Jolla
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                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
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PatentIn Release #1.0, Version #1.25
                 linear
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                                                                                                                                  (619) 535-9001
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DN: 536
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                                                                                                                                                                  P-LJ 9725
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RESULT 75
PCT-US94-12904-3
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COMPUTER: INM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/461,359
FILING DATE: 10-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
AMAE: Campbell, Cathryn A.
REGISTRATION UMBER: 31,815
REGISTRATION UMBER: 9-LJ 9725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEFHONE: (619) 535-9949
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-461-359-3
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              Sequence 3, Application PC/TUS9412904
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Takayama, Shinichi
APPLICANT: Sato, Takaaki
TITLE OF INVENTION: Bc1-2-associated proteins
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                             Query Match 0.5%;
Best Local Similarity 100.0%;
Matches 16; Conservative
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, John C.
APPLICANT: Takayama, Shinichi
APPLICANT: Sato, Takaaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Bcl-2-associated proteins
CORRESPONDENCE ADDRESS:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 733 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/152
APPLICATION NUMBER: US 08/152
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: FP-L
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Diego
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Isolated caspase recruitment domain-12 polypeptide and nucleic acids encoding them, useful for treating and diagnosing disorders associated with abnormal apoptosis such as cancer, arthritis and Alzheimer's
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     recruitment
              The sequence
                                         Claim 2; Fig 1; 93pp; English.
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                                                                                                                                                                              Bertin J, Robison KE;
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17-JUL-2000;
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                                                   The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs: from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDN/ of the invention
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2951	ggatggcttgccttcatgggtgtatttgagaatcttaagcaattagtgtttttttgacttt	2892	Оу
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2291	acatctgtaacaaacctgaaaaccttgagtattcatgacctacagaatcaacggctgccg	2232	Оу
2487		2428	
2231	aacatttattototoatggtggaagcoagtocootcaccatagaagatgagaggcacato	2172	Qy
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Isolated caspase recruitment domain-12 polypeptide and nucleic acencoding them, useful for treating and diagnosing disorders associant with abnormal apoptosis such as cancer, arthritis and Alzheimer's disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leptuberculosis; ischaemic brain injury; hypoxic brain injury; ds;
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                                                                                                                                                                                                                               Disclosure;
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The sequence represents a genomic DNA which encodes the human caspase CC recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a CC number of proteins that transmit signals that activate apoptosis and CC inflammatory pathways in response to stress and other stimuli. Therefore, C CARD-12 and its corresponding nucleic acid may be used in treatment and CC diagnosis of patients suffering from disorders associated with an CC abnormal level (an increase or a decrease) of apoptotic cell death or CC abnormal activity of stress-related pathways. The disorders include CC cancer, viral infections (e.g. systemic lupus erythematosis, arthritis), CC neurological disorders (e.g. systemic lupus erythematosis, arthritis), CC neurological disorders (e.g. Alzheimer's disease, amyotrophic lateral CC sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial CC crohn's disease, insulin-dependent diabetes, contact dermatitis, CC psoriasis, graft rejection, bacterial infections (e.g. tuberculosis, ischaemia reperfusion injury, excitotoxic brain damage, acute bacterial

Query Match
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wantibacterial; endocrine; cardiant; central nervous system; virucide;
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wantianaphylactic; haematopoietic disorder; platelet disorder; asthma;
wallergic rhinitis; diabetes; multiple sclerosis; depression;
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wallergic rhinitis; diabetes; multiple sclerosis; depression; cancer; ulcer; HIV infection; human immunodeficiency virus;

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cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiarthritic; cardiant; central nervous system; virucide; antiallergic; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vinerary; cardidiabetic; cytostatic; neuroprotective; antiallergic; antimutagen; cardidiabetic; cytostatic; neuroprotective; antisenses therapy and vaccine production, The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine conduction, The proteins and polynucleotides are useful for screening for a fisorders associated with the activity of a protein e.g. inflammation, confidential arthritis, septic shock, pancreatitis, cardiac dysfunction, concerning autoimmunity, genetic diseases, haematopoietic disorders, antiented disorders, thrombocytopaenia, wounds, burns, ulcers, cardiatis, severe combined immunodeficiency, eczema, allergic confidency; disease, parkinson's disease, neurodegenerative and concerning for steepporosis, severe combined immunodeficiency, eczema, allergic contents, disease, parkinson's disease, neurodegenerative and concerning for neurological disorders.
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cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
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N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                       AAI14389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                       taaataaagtgtactcgaagccagta
                                                                                                                                                                                        tggcaatttgatgatgatgatctcagtgttattacaggtgcttttaaactagtaactgct
                                                                                                                                                                                                                                  GAGGTCCCACAACTCGTCAAGCTTGGGTTGAAAAACTGGAGACTCACAGATACAGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                             gaggtcccacaactcgtcaagcttgggttgaaaaactggagactcacagatacagagatt
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                      #4322
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                                                                                      standard;
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                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                           (first
                      gene
                                                                                       DNA;
                                           entry)
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99.8%;
                      expression
                                                                                       421
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                                                                                       ВP
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                     analysis in human
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No. 2.1e-245;
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                     cervical cell sample
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human;

microarray; gene

expression;

cervical

epithelial cell;

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RESULT
AAI35764
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Best Local Similarity
Matches 242; Conserv
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 AAI35764;
                                                                                                                                                                                                                                                                                      2876
                          AAI35764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 421 BP;
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                                                                                           tg = tg
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                                                                                                                                                                                                                                                                                                             aggtgcatttttggaaagaaccctctgaaaaacttccagcagttgaatttggcgggaaa
                                                                                                                                               tagccaagtgttatccaagttaacttttctgcaagaagctaggcttgttggggtggcaatt
                                                                                                                                                                                                      agtgttttttgactttagtactaaagaatttctacctgatccagcattagtcagaaaact
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                                                                                                                       3057
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                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID No 4322; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to human single exon nucleic acid
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2000US-0236359.
2000GB-0024263.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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                          DNA;
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                          421
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Pred. No. 7.6e-110;
0; Mismatches 0;
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes at for antenatal diagnosis of human genetic disorders.
         AAI04213
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genetic disorder; ss.
                                                                                                                                                                                                                                  2816
                                                                                                                                                                                                                                                                                                   Sequence 421
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                                                                                                                                                                                                                                                                                                                                                                                              analyzing
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                                                                                                                                                                                                                                                7.7%;
ral Similarity 100.0%;
242; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                      genome-derived single exon nucleic acid probes useful
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                                                         421
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         standard; DNA;
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0632366
2000US-0234687
2000US-02346359
2000US-0236359
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                                                                                                                                                                                                                                                                                                   BP;
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                                                                                                                                                                                                                                                                                                                                                                                              expression in human placenta
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                                                                                                                                                                                                                                                            Score 242; DB 22;
Pred. No. 7.6e-110;
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                                                                                                                                                                                                                                                   Mismatches
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probes are useful
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Best Local :
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                                                                   2936
                                                                                                               2876
                                                                                                                                                                                                                                                                       of the breast, fibrocystic changes, proliferative bre
non-carcinoma tumours.
Note: The sequence data for this patent did not form
specification, but was obtained in electronic format
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03-AUG-2000;
                       2996
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27-SEP-2000;
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26-MAY-2000;
                                                                                                                                                                                                                                        Sequence
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                                          tagccaagtgttatccaagttaacttttctgcaagaagctaggcttgttgggtggcaatt
                                                                                                   tcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaatcttaagcaatt
                                                                                                                                   aggtgcatttttggaaagaaccctctgaaaaacttccagcagttgaatttggcgggaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-476286/51.
tagccaagtgttatccaagttaacttttctgcaagaagctaggcttgttgggtggcaatt
                                                                                       tcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaatcttaagcaatt
                                                                                                                                                                                  242;
                                                                                                                                                                                                                                                                                                                                                                                                                                              single exon
human breast
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                                                                                                                                                                                             Similarity
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease; proliferative breast disease; non-carcinoma
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe used
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                                                                                                                                                                                                                                       149 T; 0 other;
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                                                                                                                                                                                           7.6e-110;
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                                                                                                                     Query Match
Best Local Similarity
Matches 220; Conserv
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                      The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPC
            2985
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                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                          analyzing
                                                                                                                                                                                                                                                                                                                                                      Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI23590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAI23590 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe #13523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001
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                                 61
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                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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gtcagaaaacttagccaagtgttatccaagttaacttttctgcaagaagctaggcttgtt
                                           cttaagcaattagtgtttttttgactttagtactaaagaatttctacctgatccagcatta
                                                                                      | ttggcgggaaatcgtgtgagcagtgatggatggcttgccttcatgggtgtattttgagaat
                                                                          ttggcgggaaatcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaat
                                                                                                                                                                                                                                                                                                                                                                           2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                 SG,
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                                 cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ţg
                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                     genome-derived single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human;
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                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                          gene
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ilarity 100.0%;
Conservative
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microarray; gene expression;
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                                                                                                                                                                          58 A;
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                                                                                                                               Score 220; DB 22;
Pred. No. 6.2e-99;
                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                                                                                                 Rank
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                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                           cervical
                                                                                                                                                                           Т;
                                                                                                                                                                           0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cervical
                                                                                                                                                                                                                                                                                                                                          id probes useful for epithelial cells -
                                                                                                                      0;
                                                                                                                                         Length 220;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cell sample
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Best Local
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes at for antenatal diagnosis of human genetic disorders.
3045 gygtggcaatttgatgatgatgttctcagtgttattacag
                                                                                            2925
                                                                                                                           2865 ttggcgggaaatcgtgtgagcagtgatggattgcttgccttcatgggtgtattttgagaat 2924
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID No 17590; 654pp;
                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                              Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
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03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe #17590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI48904;
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                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                       121
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                                                                                                                                                               Local Similarity
les 220; Conserv
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                                                                                                              1 ttggcgggaaatcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaat 60
                                gtcagaaaacttagccaagtgttatccaagttaacttttctgcaagaagctaggcttgtt
                                                                             cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
                    gtcagaaaacttagccaagtgttatccaagttaacttttctgcaagaagctaggcttgtt
                                                                   cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
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                                                                                                                                                                                                                                                                                                                                                                                              SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gggtggcaatttgatgatgatctcagtgttattacag
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2000US-0608408.
2000US-0632366.
                                                                                                                                                               Conservative
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                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US00663
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2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; placenta; antenatal diagnosis;
                                                                                                                                                         7.0%; >--
100.0%; Pr
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                                                                                                                                                                         Score 220; DB 22;
Pred. No. 6.2e-99;
                                                                                                                                                                                                                       54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                      <u>و</u>;
                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                        single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                               English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                      76
                                                                                                                                                                                                                       Τ;
                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in human placenta sample
                                                                                                                                                                                                                                                                                                                                              probes useful
                                                                                                                                                              0,
                                                                                                                                                                                   Length 220;
                                                                                                                                                              Indels
                                                                                                                                                             0;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                 The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prohybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast tibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                       2925
                                                                      2865
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                   Claim 25;
                                                                                                                                                                                                                                                                                                                                                                          Novel single exon nucleic acid probe used to in a human breast {\mbox{\scriptsize -}}
                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                             specification, but was obtained in electronic
                                                                                                                                                                                                       Note: The sequence data for this patent did not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                            Local Sin
hes 220;
61
                                               \vdash
                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                          ttggcgggaaatcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaat 2924
cttaagcaattagtgtttttttgactttagtactaaagaatttctacctgatccagcatta
          cttaagcaattagtgttttttgactttagtactaaagaatttctacctgatccagcatta
                                                                                                                                                                                                                                                                                                                                                                                                                                   SG,
                                             ttggcgggaaatcgtgtgagcagtgatggatggcttgccttcatgggtgtatttgagaat
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                                                                                                        Similarity
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                                                                                                                                                        220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                   SEQ
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                  ID No 9197; 322pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breast disease; breast cancer;
                                                                                                                                                        58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYNAMICS INC
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                                                                                                                                                       Α;
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                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferative breast disease; non-carcinoma tumour.
                                                                                                                     7.0%;
                                                                                                                                                        32 C;
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                                                                                            Score 220; DB; Pred. No. 6.2 0; Mismatches
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                                                                                                                     DΒ
                                                                                                                                                        0 other;
                                                                                            DB 22;
5.2e-99;
es 0;
                                                                                                                                                                                                                                                                                                                                                                                     measuring
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                                                                                                                   Length 220;
                                                                                            Indels
                                                                                                                                                                                          part of the printed directly from WIPO
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                   in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13632 to AAH13632 and AAH13632 to AAH13632 and AAH13633 to AAH13632 and AAH13632 to AAH13632 and AAH13632 to AAH13632 and AAH13633 to AAH13632 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 to AAH13633 and AAH13633 and AAH13633 to AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH13633 and AAH1
                                                                                                                                                                                                                                                                                       sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3 end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5 end sequence/3 end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; SEQ ID 8287; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA clone (3'-primer) SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA;
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A, Nagai F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO:8287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto
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Dest Local :

0.6%;

Score 19; Pred. No.

43

22;

Length 549

Local

represent oligonucleotides, of the present invention

Sequence

549 BP;

162

A; 120

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119

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139 T;

9 other

Db Qy

Conservative

0;

Mismatches

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Gaps

0,

100.0%; 0.6%;

Score 19;

Pred. No.

43

19;

Length 579

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AAX30628/c
ID AAX306
Query Match
Best Local Similarity
""tohes 19; Conserva
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                                                                                                                                            Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 97 ORFS are shown. The proteins are variously cell envelope proteins, cytoplasmic proteins, secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-JUL-1997;
05-DEC-1996;
25-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine; secreted
                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Helicobacter pylori nucleic ac
products for the diagnosis, prevention and
H. pylori and other Helicobacter species
                                                                                                              Sequence 579
                                                                                                                                                                                                                                                                                                                                                                              Claims
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY11099
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19; Conser
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protein; cytoplasmic protein; cellular protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                              BP; 173 A; 130 C;
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96US-0759625.
97US-0823745.
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                                                                                                                G;
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                                                                                                              178 T; 0 other;
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ent of infection
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                                                                       AAF13098
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AAX14445/c
                                                                                                                                                      Query Match
Best Local S
Matches 19
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01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                       isolated from Helicobacter pylori and encodes a H. pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used detection and diagnosis.
  Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-)
                     13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9843478-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHPO protein;
peptic ulcer
                                          AAF13098
                                                             AAF13098 standard; cDNA; 1908
                                                                                                                                                                                                       Sequence 649 BP; 191 A; 139 C;
                                                                                                                                                                                                                                                                                                This sequence
                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1538; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                New isolated Helicobacter polynucleotides - used to develop
for the diagnosis, prevention and treatment of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                           Al-Garawi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX14445 standard;
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                                                                                                                                                      Local Similarity
nes 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pylori GHPO
                                                                                                              ACATTATTTTAACTTGAA 383
                                                                                                                                 acattatttttaacttgaa 427
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MERIEUX ORAVI
                                                                                                                                                                                                                                                                                                                                       and gastrointestinal diseases
 oryzae
                                                                                                                                                      0.6%;
llarity 100.0%;
Conservative
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pylori.
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                                                                                                                                                                                                                                                                                                represents a
                                                                                                                                                                                                                                                                                                                                                                                                            Kleanthous
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97US-0833457.
97US-0881227.
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ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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EST SEQ ID NO:5621
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                                                                                                                                                                                                                                                                                                polynucleotide of the invention.
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                                                             ВΡ
                                                                                                                                                                                                       118
                                                                                                                                                      red. No. 43
Mismatches
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                                                                                                                                                                DB
43;
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                                                                                                                                                                        Length 649;
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RESULT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 88; Page 2332; 3161pp; English.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                              oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 represent human amino acid sequences; AAB92446 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                          the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
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2000JP-0118776.
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2000JP-0241899.
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RESULT 18
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                                                                                                     Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.
                                                                                 11-NOV-1994;
                                                                                                                                                                                                Gene signature; messenger RNA; mRNA; relative abundance; frequency human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                      12-NOV-1993;
                                                                                                             01-JUN-1995
                                                                                                                                         W09514772-A1
                                                                                                                                                                                                                                                          Human gene signature HUMGS06268
                                                                                                                                                                                                                                                                                                                                                 AAT24250 standard; cDNA to mRNA; 322 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3056 tgatgatgatctcag 3073
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                      16-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences AAA31040-A32093 represent novel plant microsatellite sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New plant microsatellite markers and associated flanking species the detection of polymorphic genetic markers - \!\!\!\!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-116958/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-JUN-1998;
          (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FLET-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                     101 TGATGATGATGATCTCAG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLETCHER CHALLENGE FORESTS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 BP; 59 A; 79 C; 75 G; 60 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 140-141; 392pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%;
ilarity 100.0%;
Conservative
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                                                      93JP-0355504
                                                                                 94WO-JP01916.
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Pred. No.
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A single-stranded DNA (or its complementary strand or the corresp. Concluded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-cuntranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be constructed, as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                    Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA31416 standard; DNA; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                  Havukkala
                                                                                                              (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER. (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                        25-JUN-1998;
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                                                                                                                                                                                                                                                                          Eucalyptus grandis.
                                                                                                                                                                                                                                                                                                                                                                 Plant microsatellite marker #377.
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18; Conserv
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llarity 100.0%;
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                                                                                 ĽN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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Pred. No.
                                                                                 Glenn
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New plant microsatellite markers and associated flanking species the detection of polymorphic genetic markers -

for

Claim

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Page 188;

392pp;

English

AAA31040-A32093 represent novel plant microsatellite sequences

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RESULT 21
AAA31325/c
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Best Local
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and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3056 tgatgatgatgatctcag 3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polynucphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are
                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                          Claim 1; Page 161; 392pp; English.
                                                                                                                                                                                                                                                                                        Havukkala IJ,
                                                                                                                                                                                                                                                                                                                      (GENE-) GENESIS RES & DEV CORP LTD (FLET-) FLETCHER CHALLENGE FORESTS
                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant microsatellite marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA31325 standard;
                                                                                                                                             Sequences AAA31040-A32093 represent novel plant microsatellite sequences
                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful to locate specific economically useful genès in plant genomes
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                                                                                                                                                                                                        plant microsatellite markers and detection of polymorphic genetic
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                                                                                                                                                                                                                                                                                        Glenn M;
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                                                                                                                                                                                                                                                                                                                       & FLETCHER.
LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 T; 1 other;
                                                                                                                                                                                                           associated flanking species markers -
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3056 tgatgatgatctcag 3073

Matches Query Match Best Local :

18;

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Mismatches

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Gaps

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Similarity

0.6%;

Score 18; Pred. No.

1.3e+02; DB 21;

Length 435;

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RESULT 22
AAA3136/C
ID AAA313
XX AAA313
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Best Local S
Matches 18
                                                                         and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant microsatellite sequence; core repeat sequence; detection; pro DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
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  Sequence
                                                      useful
                                                                                                                                                                                                                                                                                                                                       Sequences AAA31040-A32093 represent novel plant microsatellite sequences
                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                   to locate specific economically useful genes
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  A; 125 C;
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Pred. No.
  146 G;
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     other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The present sequence is one of a large number of 5' ESTs derived from CC mRNAs encoding secreted proteins. No ORF has yet been conclusively CC identified within the present sequence. The 5' ESTs were prepared from CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST CC sequences usually correspond mainly to the 3' untranslated region (UTR) CC 1ibraries. Such ESTs are not well suited for isolating cDNA sequences CC derived from the 5' ends of mRNAs and even in those cases where longer CCDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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Matches 18
                      12-OCT-2001
                                                                AAI14905;
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                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
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106 ATGAATTTCATAAAGGAC 89
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18; Conservative
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                      (first entry)
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mapping; ss.
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Pred. No.
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hes 0;
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one suprobe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or stagging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 454
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cervical cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 119 A; 89 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID No 4838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DK,
                                                                                                                                                                                                                                                                                                                                                        measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%;
                                                                                                                                                                                                                                                                             placenta; antenatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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AAI04685/c
ID AAI046
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Best Loc
Matches
                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes at for antenatal diagnosis of human genetic disorders.
       Penn
                                                                                                                                                                                                                              09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                09-AUG-2001
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                            Probe; human;
                                                                                                                                                                                                            Probe
                                                                                                                                                                                                                                              AAI04685;
                                                                                                                                                                                                                                                                AAI04685 standard;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 454 BP; 119 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
                                                                                                               29-JAN-2001;
                                                                                                                                                WO200157270-A2
                                                                                                                                                                                  inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                       (MOLE-)
                                                                                                                                                                                                                                                                                                                           540
                                                                                                                                                                                                                                                                                26
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                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                           GGGGAATCTGGCAAAGGC
                                                                                                                                                                                                                                                                                                                   ggggaatctggcaaaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
       SG,
                                                                                                                                                                                                            #4676 used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                             18;
                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
       Hanzel
                                        ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                              2001WO-US00661
                                                                                                                                                                                   disease;
                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US00663
                                                                                                                                                                                         breast disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression
       DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DK,
                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                            measure gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4943; 654pp;
                                                                                                                                                                                                                                                                                                                                                    0.6%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
       Chen
                                                                                                                                                                                  proliferative breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                                                                          557
                                                                                                                                                                                                                                                                454
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                            breast
                                                                                                                                                                                                                                                                                                                                                                                        110 G;
       Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                 18;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
                                                                                                                                                                                                                                                                                                                                                                                        136 T;
                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                   1.3e+02;
                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                        0 other;
                                                                                                                                                                                            development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes useful
                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                           Length 454;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                            breast sample
                                                                                                                                                                                                                                                                                                                                                                                                                                         probes
                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                 ng gene
                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          (SENP).
                                                                                                                                                                                                                                                                                                                                                                                                                  useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammantory diseases of the breast diseases and non-carcinoma tumnours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                    6081
                                                                                 New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                                                              06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel single exon nucleic acid probe used in a human breast -
                                                                        diagnostic,
                                                                                                                                                                                               26-FEB-1999;
                                                                                                                                                                                                                     21-FEB-2000;
                                                                                                                                                                                                                                         06-SEP-2000
                                                                                                                                                                                                                                                               EP1033401-A2
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                        Human secreted
                                                                                                                                                                                                                                                                                                                                                                                   AAC01809;
                                                                                                                                                                                                                                                                                                                                                                                                        AAC01809 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                          (GEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540 ggggaatctggcaaaggc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention relates to novel single exon nucleic acid present sequence is one such probe. The probes are useful for
                                                                                                                               2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGAATCTGGCAAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-476286/51.
                                                                                                                                                                                                                                                                                                       therapy;
                                                                                                                                                    Milne Edwards
                                                                                                                                                                                                                                                                                                                   ű
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
18; Conserv
                                                                                                                    AAG01803
                                                                                                                                                                          GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 BP; 119 A;
                                                                                                                                                                                                                                                                                                                  EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID No
                                                                         forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                     2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                         chromosome mapping;
                                                                                                                                                                                                                                                                                                                   expressed sequence
                                                                                                                                                                                                                                                                                                                                        protein 5' EST,
                                                                                                                                                                                               99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                        cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%;
                                                                                                                                                    Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4676; 322pp; English.
                                                                        gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 C;
                                                                                                                                                    Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                        466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score Pred.
                                                                                                                                                                                                                                                                                                                                                                                                        ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 G;
                                                                                                                                                                                                                                                                                                                                         SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                         tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
No.
                                                                         and chromosome
                                                                                                                                                    Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 T;
                                                                                                                                                                                                                                                                                                                                         NO:
                                                                                                                                                                                                                                                                                                                   secreted
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1.3e+02;
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                                                                                                                                                                                                                                                                                                                                         1807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                  tag (5' EST) for to 5'ESTs and for
                                                                        mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454;
                                                                                                                                                                                                                                                                                                                    cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          where the probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                      for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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sequence. ....

30

different tissues.

EST sequences

usually

correspond

the

Claim

1:

SEQ

IJ

1807;

71pp

+ CD-ROM;

English.

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within t sequence. The 5' ESTs were prepared from total human RNAs or polyA+R

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AAA31287/c
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Best Local
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Sequences AAA31040-A32093 represent novel plant microsatellite sequences and associated flanking species. The sequences comprise a central core repeat sequence, especially selected from the sequences AAA32094-A32096 with left and right flanking sequences. The polynucleotide sequences can be used in the detection of DNA polymorphisms, in genome mapping, in physical mapping, in positional cloning of genes, in variety identification and in evaluation of genetic variability within and between plant tissues, populations, cultivars, species and species groups. They may also be used to design hybridization probes for oligonucleotide fingerprinting and library screening and to design primers for microsatellite-primed PCR. Microsatellite markers are useful to locate specific economically useful genes in plant genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                             Claim 1; Page 149; 392pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-116958/10
                                                                                                                                                                                                                                                                                                                                                                                                                              Havukkala IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant microsatellite sequence; core repeat sequence; detection; probe; DNA polymorphism; genome mapping; physical mapping; fingerprinting; variety identification; genetic variability evaluation; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09967421-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant microsatellite marker #248.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287/c
AAA31287 standard; DNA; 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENESIS RES & DEV CORP LTD & FLETCHER. (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           766 ttttccttcttgatggct 783
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                                                                                                                                                                                                                                                                                                                plant microsatellite markers and associated flanking species for detection of polymorphic genetic markers - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                           Bloksberg LN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-NZ00092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Α.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 C;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                              Glenn M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; I
1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Sequence

468

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143

agaaggtggagcaggatg 160

166 agaaggtggagcaggatg 183

Query Match Best Local : Matches

l Similarity 18; Conserv

Conservative

0;

Mismatches

Indels

0,

Gaps

0;

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Score 18; Pred. No.

DB 22;

Length 472;

1.3e+02;

0.6%;

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AAI11787
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Best Local
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                          03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                         (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                       expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3056 tgatgatgatgatctcag
  Sequence 472 BP; 129
                                                                                                                                                The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                            Claim 25;
                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                              WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                            04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #1720 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI11787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI11787 standard; DNA; 472
                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 TGATGATGATGTCTCAG 84
                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                          SEQ ID No 1720; 487pp;
                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                         2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                              2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08; 1
A; 77 C; 153 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                        Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                            English.
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1.3e+02;
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Best Local S
Matches 18
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes of the present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying go expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                           WPI;
              Probe; human; inflammatory
                                     Probe #1709
                                                    09-OCT-2001
                                                                   AAI01718;
                                                                                  AAI01718 standard;
                                                                                                                                                                                         Sequence 472
                                                                                                                                                                                                                                                    Claim 25; SEQ ID No 1787; 654pp; English
                                                                                                                                                                                                                                                                    analyzing
                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                       (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                    26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; microarray; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI33101 standard; DNA; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI33101;
                                                                                                                       143
                                                                                                                                      166
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                                                                                                                      agaaggtggagcaggatg 160
                                                                                                                              agaaggtggagcaggatg 183
                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                                                                                                                                                           2001-488897/53.
                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #1787 used
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder;
                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                     2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234639.
2000US-023639.
                                     used to
                                                                                                                                                     Conservative
             breast disease; breast cancer; development disorder disease; proliferative breast disease; non-carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US00663
                                                   (first
                                                                                                                                                                                          BP; 129 A; 77 C; 153 G; 113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to measure
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS.
                                                                                  DNA; 472
                                                                                                                                                  0.6%; 50
100.0%; Pr
                                    measure gene expression
                                                   entry)
                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     placenta; antenatal diagnosis;
                                                                                  BP
                                                                                                                                                    Score 18; DB; Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                            DB 22;
1.3e+02;
                                    in human breast sample
                     development disorder;
                                                                                                                                                                                                                                                                           probes useful
                                                                                                                                                     0;
                                                                                                                                                                  Length 472;
                                                                                                                                                     Indels
                                                                                                                                                     0;
                                                                                                                                                                                                                 are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sample
                                                                                                                                                     Gaps
                                                                                                                                                                                                                        gene
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               tumour
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Best Local S
Matches 18
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                        Penn
06-MAR-1989;
              05-MAR-1990;
                                                          Ovis ammon aries
                                                                         Ovine placental lactogen; ds;
                                                                                       Sequence
                                                                                                       07-JAN-1991
                                                                                                                      AAQ05868;
                                                                                                                                                                                                                                             Sequence 472 BP;
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                            12-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                         2001-476286/51.
                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                                         . Similarity
18; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
89US-0319585
              90EP-0302322
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed aspecification, but was obtained in electronic format directly from WIPO
                                                                                                                                              AAQ05868 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel single exon nucleic in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                      143 agaaggtggagcaggatg 160
                                                                                                                                                                                                                                                                                  166 agaaggtggagcaggatg 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
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encoding mamalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                (first entry)
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2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID No 1709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 A; 77 C; 153 G;
                                                                                                                                                                                                                                                                                                                                                                            0.6%;
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                                                                                                                                              594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322pp; English.
  growth hormone
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                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 T;
                                                                                                                                                                                                                                                                                                                                                                            DB 22; 1
  receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to measuring gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
                                                                                                                                                                                                                                                                                                                                                        0,
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  protein
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Best Local
                                                                                                                                                                                                                                                                                                           Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombina culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative expression of the same genes in one or more second filamentous fungal
                                                Claim
                                                                               Monitoring differential expression of genes in filamentous uses fluorescence-labeled nucleic acids isolated from the
                                                                                                                 WPI; 2000-594572/56.
                                                                                                                                                                                                                      22-MAR-2000; 2000WO-US07781
                                                                                                                                                                                                                                            28-SEP-2000
                                                                                                                                                                                                                                                                                       Fusarium venenatum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence encoding growth-hormone-receptor-binding protein useful for increase of mammalian meat and milk prodn. and
                                                                                                                                                                                                22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                         Multiple gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF07589 standard; cDNA; 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 594 BP; 191 A; 150 C; 125 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-276995/37.
                                                                                                                                                              (NOVO ) NOVO NORDISK BIC
                                                                                                                                                                                                                                                                                                                                                                                 Fusarium venenatum EST SEQ ID NO:112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to ovine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         production and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WI,
                                                                                                                                          RM,
                                            86; Page 419; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding protein may be used to increase meat and milk
on and decrease fat content especially in sheep and gos
shows an identity of 26% with human growth hormone and
placental lactogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in fat content.
                                                                                                                                        Rey MW,
                                                                   of expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colosi PC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                         NORDISK BIOTECH
                                                                                                                                                                                                99US-0273623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22pp; English.
                                                                                                                                         Shuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%;
                                                                                                                                                                                                                                                                                                                                                          filamentous
                                                                                                                                        JR,
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128
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hes 0;
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                                                                                                                                         Clausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 594;
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                                                                                                                                        IG,
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cells an
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and 67%
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AAC44321/c
ID AAC44321 standard; DNA; 682
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Best Local
25-FEB-1999

05-MAR 1999

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23-MAR-1999

25-MAR-1999

25-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

21-APR-1999

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23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF11879 to AAF11837 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2127
                                                                                                                                                                                                                                                                                                                                                                                                 metabolic pathway; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                               25-FEB-2000;
                                                                                                                                                                                                                                                                                                           06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                             2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
99US-0128714.
99US-0129845.
99US-0130077.
99US-0130449.
99US-0130510.
99US-0130891.
99US-0131449.
99US-0131449.
99US-0132048.
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99US-0128234.
                                                                                                                                                                      99US-0126264.
99US-0126785.
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                                                                                                                                                                                                                  9908-0123548
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                    termination sequence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO:
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26-OCT-1999
       The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
oligonucleotide
                                                                                           Primer sets for synthesizing polynucleotides, parti-
full-length cDNAs defined in the specification, and
and/or diagnosis of the abnormality of the proteins
                                                                                                                                                             0ta
                                                                                                                                                                                                         11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                           29-JUL-1999;
27-AUG-1999;
                                                                 Claim
                                                                                                                                  WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                          07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                        AAH05406;
                                                                                                                                                                                                                                                                                                                                                                                                          AAH05406 standard;
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                                                                                                                                                                                                                                                                                                                                primer;
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                                                                                                                                                   Isogai T,
Sugiyama
                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                    clone
                                                                                                                                                                                                 2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                ID 2241;
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                        2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0161404
99US-0161405
99US-0161406
99US-0161350
99US-0161350
99US-0161361
99US-0161361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                detection; diagnosis;
                                                                                                                                                                                                                           99JP-0248036
99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -Sn66
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                                                                                                                                                                                                                                                                                                                                                 (5'-primer) SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                          cDNA;
                                                                                                                                                            Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%;
                                                               2537pp +
                                                                                                                                                   hikawa T,
Wakamatsu
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s defined
least 15
                                                                                                   polynucleotides, particularly the 5602 the specification, and for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18;
Pred. No.
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                                                                                                                                                   Hayashi K,
A, Nagai K
                                                                ROM;
                                                                                                                                                                                                                                                                                                                                                   NO:2241.
                                                                                                                                                                                                                                                                                                                               antisense therapy; gene
                                                                                                                                                   Nagai K,
in the specification, nucleotides; or (b) a
                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                            Saito
                                                                                                                                                   otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 682;
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                                                                                                                                                            Yamamoto
                                                                                           detection by the
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                                                                                                                                                                                                                                                                                                                               therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC of an oligonucleotide comprising a sequence complementary to the C complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC in gene therapy. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC etaction and/or diagnosis of the abnormality of the proteins encoded by CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB13633 to AAH18742 represent human cDNA sequences; AAB92446 to CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 CC represent oligonucleotides, all of which are used in the exemplification of the present invantion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                   14-NOV-1997;
06-MAY-1997;
16-MAY-1997;
The present sequence represents a gene isolated from Enterococcus faecalis. The present invention describes genes, p and antigenic polypeptides isolated from E. faecalis. The prote be used in vaccines for preventing or attenuating an infection by a member of the Enterococcus genus in an animal. They can all used for detecting Enterococcus antibodies in a sample. The nuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis; i
detection; attenuation;
                                                                                                  Claim
                                                                                                                              tor
                                                                                                                                             products for
                                                                                                                                                        New isolated
                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                          04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                WO9850554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus
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                                                                                                                                                                                                                                                        ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998
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                                                                                                                              prevention
                                                                                                                                                                                    1999-070095/06
DB; AAY00222.
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                                                                                                                                                                                                                                                        HUMAN
                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                           the detection of Enterococcus
                                                                                                                                                        Enterococcus faecalis polynucleotides - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                  212;
                                                                                                                                                                                                                                                          GENOME SCI INC
                                                                                                                                                                                                                                                                                   97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                              or attenuation
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                                                                                                301pp;
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                                                                                                                                                                                                                             Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection;
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                                                                                                 English.
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                                                                                                                              Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine;
                                                                                                                                                                                                                              Kunsch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; 1
1.4e+02;
                                                                                                                                           and for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune response; diagnosis;
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proteins can
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1999;
07-APR-2000;
03-AUG-2000;
                                    analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                      Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C glutamicum
                                                                                                                                              sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and
                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                              P-PSDB; AAG91867.
                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                    Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-2000; 2000EP-0127688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium
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                                                                                                                                                                                       The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUN-2001
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                                                                                                                                                                                                                  8; SEQ ID NO: 2121; 246pp + Sequence Listing; English
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                            Patent Office.
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                                                                                                                                                                                                                    Mizoguchi H,
Senoh A, Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting
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da M, Ozaki A;
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Pred. No.
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ntion can also be used for screening
and antagonists of E. faecalis prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G;
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1.4e+02;
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Sequence

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other;

AAZ52527/c
ID AAZ525
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AC AAZ525
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AAZ52527 standard;

cDNA;

1034

ВP

AAZ52527

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                                        Query Match
Best Local :
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Best Local Similarity
Matches 18; Conserv
                                 Matches
                                                                                          Receptor binding protein may be used to increase meat and milk production and decrease fat content especially in sheep and got Sequence shows an identity of 26% with human growth hormone and to owine placental lactogen.

Sequence was obtained using probe described in AAQ05869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3040 ttgttgggtggcaatttg
                                                                                                                                                                                              WPI; 1990-276995/37.
P-PSDB; AARO6643.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ05870 standard;
                                                                          Sequence
                                                                                                                                             Claim 14;
                                                                                                                                                             decrease in fat content.
                                                                                                                                                                     DNA sequence encoding growth-hormone-receptor-binding useful for increase of mammalian meat and milk prodn.
                                                                                                                                                                                                                                                         06-MAR-1989;
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                                                                                                                                                                                                                                                                                          12-SEP-1990
                                                                                                                                                                                                                                                                                                          EP386979-A.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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(GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                            ammon
                                                                                                                                                                                                                                                                                                                                                                            placental lactogen;
                                 . Similarity
18; Conserv
                                                                          992
                                                                                                                                                                                                                                                                                                                                                                                            encoding mamalian growth
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                                                                                                                                                                                                                       Colosi
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Pred. No.
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Pred. No.
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1.4e+02;
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29-FEB-2000

(first entry)

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Query Match
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29-SEP-1998;
09-OCT-1998;
                                                                                                                                                                       vaccines) or suppressing activity, haematopolesis regulating activity, tissue growth activity, activity/inhibin activity, chemotactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. Therapeutic compositions are also presently valuable for veterinary applications. AAX52475 to AAX52581 encode human secreted proteins, and AAY73500 to AAY73500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-FEB-1999;
06-APR-1999;
13-MAY-1999;
                                                                                                                                                                                                                                                                                         polynucleotides obtained from adult testes, foetal brain, adult brain, brain, (foetal and adult), foetal kidney, adult spleen, and adult thymus cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  make
                                                                                                                                   Sequence 1034 BP; 305 A; 228
                                                                                                                                                                                                                                                                                                                                                                           The present invention describes human secreted proteins encoded polynucleotides obtained from adult testes, foetal brain, adult
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31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; immunostimulatory; haemostatic; cytok proliferative; differentiative; chemotactic; chemokinetic; vacthrombolytic; antiinflammatory; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions in humans or animals
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17-AUG-1998;
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Novel
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                                                                                                                                                                human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                       Page 653;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0102329.
98US-0103615.
98US-0111799.
98US-0112159.
98US-0114415.
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99US-0287150.
99US-0311021.
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98US-0102329
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                                                                                                                                                             proteins, given in
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Pred. No.
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                                                                                                                                  222 G;
                                                            Mismatches
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                                                                           1.4e+02;
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                                                                                                                                  3 other;
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                                                                                                                                                              present invention
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to AAF71750 encode the Corynebacterium glutamicum sugar

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RESULT 40
AAF71387
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03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
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27-AUG-1999;
31-AUG-1999;
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09-JUL-1999;
09-JUL-1999;
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08-JUL-1999;
08-JUL-1999;
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08-JUL-1999;
08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum; carbon metabolism and energy production; SMP protein; sugar metabolism and oxidative phosphorylation protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
                 Claim 3;
                                    New isolated Corynebacterium glutamicum nucleic acid encoding a metabolism and oxidative phosphorylation protein for production modulation of production of fine chemicals e.g. amino acids, carbohydrates or enzymes -
                                                                                       P-PSDB;
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14-JUL-1999;
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08-JUL-1999;
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                                                                                                                   Pompejus M,
                                                                                                                                        (BADI )
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                                                                                                 2001-061975/07
                                                                                                                                         BASE
                                                                                        AAB79270.
                 Page 217-219; 1246pp; English
                                                                                                                    Kroeger
                                                                                                                                        AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-IB00943
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99DE 1040765.

99US-0151572.

99DE-1042076.

99DE-1042079.

99DE-1042087.

99DE-1042088.

99DE-1042088.

99DE-1042088.

99DE-1042123.

99DE-1042123.
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99DE-1031420.
99DE-1031424.
99DE-1031428.
99DE-1031431.
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99DE-1031634.
99DE-1032180.
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99US-0143208.
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99DE-1031413
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RESULT 4
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AC AAZ4
AC AAZ4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 18
                 This invention describes novel polypeptide fragment sequences (I) and their encoding nucleic acids (II) which are highly expressed in normal bladder tissue and have cytostatic activity. (II) are used for recombinant expression of (I) and to isolate complete genes. (I) are used to identify agents suitable for the treatment of bladder tumours, to directly treat this form of cancer (including expression from gene therapy vectors), or are used in a preparation for cancer treatment. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3040 ttgttgggtggcaatttg 3057
                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                       New polypeptides and their nucleic acids, useful bladder tumour and identification of therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE19818620-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bladder; treatment; EST; expressed sequence tag; cytostatic;
cancer; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1998;
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DB; AAY60559, A
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                                                                                                                                                                                                                                                    Page 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (i.e.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Specht T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-1018620
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                                                                                                                                                                                                                                                                                                                                                                                           AAY60560,
                                                                                                                                                                                                                                                 366pp;
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  generation
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                                                                                                                                                                                                                                                    German.
                                                                                                                                                                                                                                                                                                                                                                                             AAY60561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
  of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Β,
  specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schmitt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
1.4e+02;
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                                                                                                                                                                                                                                                                                                       agents
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  (II)
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RESULT 4
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, and therefore reduces the number of failures because of ESTs from different libraries representing different parts of the same unknown gene distorting the estimated frequency of occurrence in a particular tissue. AAZ4212-Z42248 represent EST fragments derived from a human normal bladder tissue cDNA library which encode the protein fragments represented in AAY60329-Y60591.
                              inserted in a suitable vector and expressed in a transformant of a suitable organism such as E.coli HMS-174 or HB-101 or a yeast. It is new so are a SP of human myeloid cell origin; precursors of SP having an N-terminal splittable or signal peptide; and a transcription-controlling DNA sequence required for expression of the gene. SP has antithrombotic activity, esp. useful in disseminated intravascular coagulation. By expression of the protease gene in a suitable transformant organism SP
                                                                                                                                                                                                                                                                                   09-SEP-1987;
05-MAR-1987;
Sequence
                                                                                                                          SP DNA
                                                                                                                                                Disclosure;
                                                                                                                                                                        useful
                                                                                                                                                                                                             WPI; 1988-271161/38.
                                                                                                                                                                                                                                    Aoki Y,
                                                                                                                                                                                                                                                           (TORA)
                                                                                                                                                                                                                                                                                                                       26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                 07-SEP-1988
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription (SP) of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-1991
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                        obtained
                                                                                                                        is selected and cloned from a human myeloid cell library,
                                                                                                                                                                       protease of human myeloid
in disseminated intravasc
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                                                                                                                                                                                                                                                                                                                                                                                                                                             myeloid
 BP;
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87JP-0050676
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                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                       myeloid cell; intravascular coagulation treatment;
305
                      large quantity.
                                                                                                                                                                                                                                   Naruto M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
                                                                                                                                             52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%;
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                             region of gene encoding serine protease cell origin.
                                                                                                                                                                        intravascular
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Pred. No.
                                                                                                                                                                                                                                    Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338
 385
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                                                                                                                                                                                     cell
G;
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coagulation
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Τ,
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other
                                                                                                                                                                        treatment
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Query Match Best Local S Matches 18

l Similarity 18; Conserv

Conservative

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Mismatches

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Gaps

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Score 18; Pred. No.

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Length 1250

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RESULT 43
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                       catggtcatcgtcaccac
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                                                  0.6%; >--
100.0%; Pr
                                                             Score 18;
Pred. No.
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                                                             DB 21;
1.4e+02;
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                                                                   Length 1473;
                                                     Indels
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Esterase; flea; protective immune response; carboxylesterase; haematophagous ectoparasite infestation; nfE51515; ds.
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RESULT

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arthropod;

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RESULT 4
AAV40737/
ID AAV4
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AC AAV4
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DT 23-S
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KW Este
KW haem
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ID AAA47150 standard; DNA; 1491
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Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a serine protease inhibitor protein. The protein is isolated from the green-lipped mussel (Perna canaliculus) and exhibits, inter alia, anti-thrombin activity and divalent metal cation binding activity. The serine protease inhibitor protein has a molecular weight of about 55 kilo Daltons. The protein, and its fragments, are useful in medicaments, in food, as dietary supplements or as bioremediation agents. In the dietary supplements, the protein is associated with or bound to at least one divalent cation (such as calcium, magnesium or zinc) of dietary significance. The proteins or their fragments are also useful as
                                                                                                                                                                                                                                                                                                1051 tctttgtggtcatcactt 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Perna canaliculus serine protease inhibitor protein exhibiting anti-thrombin activity and divalent metal cation binding activity, useful as an anticoagulant agent and as a dietary supplement -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease inhibitor; green-lipped mussel; anti-thrombin; divalent metal cation binding activity; dietary supplement; anticoagulant; ss.
                                                         C. felis esterase, nFE51515, coding sequence
                                                                                                  23-SEP-1998
                                                                                                                                         AAV40737;
                                                                                                                                                                              AAV40737
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1491 BP; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anticoagulant agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 9-10; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-452375/39.
P-PSDB; AAY93750.
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23-JUL-1999;
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                                                                                                                                                                              standard;
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                                                                                                (first entry)
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99NZ-0336906
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100.0%; Pr
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Pred. No.
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1.4e+02;
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AAV40738
SXCCCCCCCCCCCCCCX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes the flea esterase protein, nfE51515 (the complementary strand is shown in AAV40738), of the invention. When administered to animals, the protein induces a protective immune cadministered to animals, the protein induces a protective immune compositions containing CE proteins, are used, therapeutically or as vaccines, to protect particularly mammals and birds, specifically cats and dogs, against haematophagous ectoparasite infestation (HEP), compositions containing the proteins are used, therapeutically cats and dogs, against haematophagous ectoparasite infestation (HEP), compositions can be used to treat carthropods generally, including pests of agricultural crops, trees, cc stored goods etc., also those that are vectors of disease. Fragments of the DNA can be used as probes and primers for identification or compounds to the DNA can be used as probes and primers for identification or compounds to a protein and to target cytotoxic compounds to HEP. The compounds containing CE are effective against both adult and larval stages; they can be used development, metamorphosis, feeding, digestion and reproduction.
                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                       Ctenocephalides
                                                                                                                                            C. felis esterase, nFE51515, coding sequence complementary strand
                                                                                                                                                                                                                                                                                                                                                1002 ctccaaattcagaaatcc 1019
              22-MAY-1998
                                          WO9821324-A1
                                                                                                                   Esterase; flea;
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                                                                                                                                                                                                              AAV40738;
                                                                                                                                                                                                                                         AAV40738 standard; cDNA; 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding carboxyl:esterase(s) from fleas - useful, e.g. in vaccines, for preventing infestation by haematophagous
                                                                                                   haematophagous
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1515 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ectoparasites, particularly on cats and dogs
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P-PSDB; AAW57852.
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                   ectoparasite infestation;
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                                                                                                 protective immune response; carbox;
ectoparasite infestation; nfE51515;
                                                                        felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
                                                                                                                                                                                                                                                                                                                                                                                            0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wisnewski N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 C;
                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 G;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                            DB 19; 1
1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Τ;
                                                                                                                 carboxylesterase; arthropod;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 other;
                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                          Length 1515;
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                   ds
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            0;
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Query Match
Best Local Similarity
"~+~hes 18; Conserva
RESULT 47
AAF21032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     СÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specifically fleas. More generally the compositions can be used to treat arthropods generally, including pests of agricultural crops, trees, stored goods etc., also those that are vectors of disease. Fragments of the DNA can be used as probes and primers for identification or production of nucleic acid. Antibodies against the protein can be used for passive immunisation; to screen expression libraries; to isolate the protein and to target cytotoxic compounds to HEP. The compounds containing CE are effective against both adult and larval stages; they target CEs, including juvenile hormone, that are involved in development, metamorphosis, feeding, digestion and reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
                                                                                                                                                                                                                                                             human; airway disorder; bronchoconstriction; lung inflammation;
surfactant depletion; respiratory; bronchodilator; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1002 ctccaaattcagaaatcc 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protective immune (antibody) response against carboxylesterase (CE), so they, or compositions containing CE proteins, are used, therapeutically or as vaccines, to protect particularly mammals and birds, specifically cats and dogs, against haematophagous ectoparasite infestation (HEP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the complementary strand of the DNA encoding the flea esterase protein, nfE51515 (see AAV40737 for coding strand), of the invention. When administered to animals, the protein induces a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 115-116; 230pp; English
                                                                                        Homo sapiens.
                                                                                                                                               chronic
                                                                                                                                                                 pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                        Human low adenosine antisense oligonucleotide related sequence #2599
                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    AAF21032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF21032 standard; DNA; 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ectoparasites, particularly on cats and dogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding carboxyl:esterase(s) from fleas - useful, e.g. in vaccines, for preventing infestation by haematophagous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brandt KS, Silver GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1997;
                                                                                                                                                                                                                                                                                                  LOW adenosine antisense oligonucleotide; phosphorothioate; allergy;
                                                                                                                                             obstructive pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US20598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 A; 314 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%;
                                                                                                                                                                   emphysema; pulmonary transplantation rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wisnewski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18;
Pred. No.
                                                                                                                                             disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 G; 504 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4e+02;
                                                                                                                                                                                                                                                                             lung inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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WO200062736-A2

24-MAR-2000;

2000WO-US08020

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RESULT 4
AAA34910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

CC The antisense oligonucleotides and (1) can be used to down-regulate the cc expression and or activity of target polypeptides associated with activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and communoglobulins and antibodies, antibody receptors, cytokines and communoglobulins and antibodies, antibody receptors, cytokine and cc chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors bradykinin receptors, cytokine and cc receptors, cytokine and cc receptors, communoglobulins, and peripheral nervous and non-nervous system creceptors, cytokine and cc receptors, solventh factors, vasoactive peptides and creceptors, cytokine and cc receptors, communities, defensins, growth factors, vasoactive peptides and creceptors, defensins, growth factors, vasoactive peptides and creceptors, binding proteins and malignancy associated proteins. The creceptors, binding proteins and malignancy associated proteins. The creceptors oligonuclectides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction cand/or bronchoconstriction) and/or lung inflammation, allergy(ies) cc and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, callergies, asthma, impeded respiration, respiratory distress syndrome conversation, emphyseman, chronic obstruction value nulmonary vasoconstriction, pulmonary disease (CDP), pulmonary disease (CDP).
                                                                                                                                                                                                                                                       Ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; infilammation; allergy; allergic altergic bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway
                                                                                                                                                                                                                                                                                                                                                                                           1081 tgggtgaaagtgagttcc 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1561 BP; 354 A; 445 C; 485 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 840; 1592pp; English.
                                                                                                                   Human
                                                                                                                                                                                                                                                       AAA34910 standard; DNA; 1561 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. ARF18434 to ARF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Low adenosine (A) content antisense oligonucleotides which trigger adenosine receptors during metabolism, useful e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-679539/66
                                                                                                                                                             28-JUL-2000
                                                                                                                                                                                                             AAA34910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYEC-) UNIV EAST CAROLINA (NYCE/) NYCE J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                 142 tgggtgaaagtgagttcc 159
                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                 adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0127958
                                                                                                                 receptor related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                 polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1561;
                                                                                                                 ij
                                                                                                                   NO:2599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
Disclosure; Page 769; 1343pp; English
                                                                         cancers
                                                                                                                                                                                                                                      WPI; 2000-205971/18
                                                                                                                                                                                                                                                                                                                                                                   (UYEC-) UNIV EAST CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200009525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0095212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US17712
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RESULT 49
AAH13702/c
ID AAH137
XX
AC AAH137
XX
AC AAH137
XX
DT 26-JUN В Š The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which care targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analyssic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. is chaemic conditions, pulmonary vasoconstriction, allergies, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (OPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of decayadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32312 represent the Query Match Best Local : Matches 1081 tgggtgaaagtgagttcc 1098 nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32923 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequence AAH13702 standard; AAH13702; Sequence 1561 BP; 354 A; 445 C; 142 tgggtgaaagtgagttcc 159 Similarity the sequence listing. Conservative cDNA; 1579 0.6%; 0; Score 18; Pred. No. ВP 485 Mismatches G; 277 T; 0 DB 21; 1.4e+02; Length 1561; other; Indels 0; Gaps

0

26-JUN-2001

(first entry)

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RESULT 50
AAQ12528/c
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                   sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 13 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                            AAQ12528 standard;
                                                                                                                                                      1229 ATGAATTTCATAAAGGAC 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 10578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; primer;
                                                                                                                                                                          36 atgaatttcataaaggac 53
                                                                                                                                                                                                                                                                                                                                                                                        present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Nishikawa T,
, Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                1579
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2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-0248036
                                                                                                                                                                                                                                                                                                                                              468
                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
                                                                                                                                                                                                                                                          0.6%;
                                                                                                                                                                                                                                                                                                                                              Α,
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                                            1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IJ
                                                                                                                                                                                                                                                                                                                                              274
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                                                                                                                                                                                                                                        0;
                                            ВP
                                                                                                                                                                                                                                                          Score 18;
Pred. No.
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                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                            283 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K,
A, Nagai K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagai K,
                                                                                                                                                                                                                                                                                                                                            554
                                                                                                                                                                                                                                                        DB 22; 1
1.4e+02;
                                                                                                                                                                                                                                                                                                                                            Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito K, Y, Otsuki T;
                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                           Length 1579;
                                                                                                                                                                                                                                                                                                                                              other
                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a combination
                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                            RESULT
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Matches
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AAQ12528

Key

Location/Qualifiers

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AAA47151/c
ID AAA47151 standard; DNA; 1611
                                                                                                                                                                                                                                                                                                                         Query Match
                                  Serine protease inhibitor; green-lipped mussel; anti-thrombin; divalent metal cation binding activity; dietary supplement;
                                                                      DNA encoding
                                                                                                                        AAA47151;
                                                                                                                                                                                                                                                                                                                        Sequence 1611 BP;
                                                                                                                                                                                                                                                                                                                                                heterologous DNA, encoding metabolic enzymes, to engineer cells to express thymidine deoxyribonucleosides (TdNs) in amts, providing a fermentation source of TdNs. see also AAQ12526-27.
                                                                                                                                                                                                                                                                                                                                                                                             The sequence, comprising flanking DNA sequences obtd. from a PBS1 bacteriophage, encodes an enzyme capable of converting a thymidine deoxyribonucleoside monophosphate to a thymidine deoxyribonucleoside monophosphate to a thymidine deoxyribonucleoside. The sequence may be used together with metabolic mutations of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 7(a-c); 79pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microorganism contg. causing accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mc Dandliss RL,
Perna canaliculus.
                                                                                                03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recoverable amts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis CMG356 (ATCC 33234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHEM-) CHEMGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deoxyribonucleic acid; thymidine; dTMP; pyrimidine;
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                                                                                                                                                                                                                          343 aggatttaaaggacttgt 360
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DB; AAR12555.
                                                                                                                                                                                                             AGGATTTAAAGGACTTGT
                                                                                                                                                                                                                                                              l Similarity
18; Conser
                                                                                                                                                                                                                                                              Conservative
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                       cation
                                                                      serine protease inhibitor protein
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136..857
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                                                                                                                                                                                                                                                                                                                         683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            deoxyribonucleic acid - encoding enzyme
  of pyrimidine deoxyribonucleoside in
                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                    0.6%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                        244 G;
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                        513
                                                                                                                                                                                                                                                                                    DB 12;
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                                                                                                                                                                                                                                                                                                                        other;
                                                                                                                                                                                                                                                                                    Length 1611;
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AAA15908/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein. The protein is isolated from the green-lipped mussel (Perna canaliculus), and exhibits, inter alla, anti-thrombin activity and divalent metal cation binding activity. The serine protease inhibitor protein has a molecular weight of about 55 kilo Daltons. The protein, and its fragments, are useful in medicaments, in food, as dietary supplements or as bioremediation agents. In the dietary supplements or as bioremediation agents. In the dietary supplements, the protein is associated with or bound to at least one divalent cation (such as calcium, magnesium or zinc) of dietary significance. The proteins or their fragments are also useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scotti PD,
                                                           allergic reaction; osteoporosis; osteoarthritis; periodontal disease; nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion inju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1611 BP; 499 A; 348 C; 360 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Perna canaliculus serine protease inhibitor protein exhibiting anti-thrombin activity and divalent metal cation binding activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY93750.
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23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-2000
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        systemic cytokine damage; tissue differentiation; contraceptive; coagulation disorder; myocardial infarction; inflammatory conditiseptic shock; sepsis; ischaemia; reperfusion injury; arthritis; t
                                                                                                               multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
                                                                                                                             cytokine production; cell proliferation; cell diffinumume deficiency; infectious disease; autoimmune
                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                   AAA15908 standard; cDNA; 1619
                                                                                                                                                                                                                                                                                                                                                                                                                   1051 tctttgtggtcatcactt 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anticoagulant agents.
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                                                                                                                                                                                                                                                                                                                                                                                     767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   TCTTTGTGGTCATCACTT 750
                                                                                                                                            protein; hydrophobic domain; nutritional source; haematopoiesis;
lne production; cell proliferation; cell differentiation;
                                                                                                                                                                                                protein clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as an anticoagulant agent and as a dietary supplement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 10-11; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dearing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                 (first entry)
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/product= 1557..1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                HP10195 full length coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encodes a serine protease inhibitor is isolated from the green-lipped m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Greenwood DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No.
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                                                                                                                                disorder;
                               condition;
                                                                                                                                asthma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity
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                                              Stroke
                                                                injury
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Best Local Similarity Matches 18; Conserv

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Score 18; Pred. No.

DB 21; 1.4e+02;

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Sequence

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                                                                                                                                                                                                                                                                                                                     CC immune stimulating or immune suppressing activity. It can be used in the creatment of various immune deficiencles and disorders, and to treat confectious diseases caused by viral, bacterial, fungal or other confectious. The protein is also used for treating autolimmune disorders conditions. The protein is also used for treating autolimmune disorders conditions multiple sclerosis, systemic lupus erythematosus, and rheumatoid conditions such as asthma, and in immune suppression after organ conditions such as asthma, and in immune suppression after organ and consequently in the treatment of myeloid or lymphoid cell cand consequently in the treatment of myeloid or lymphoid cell conditions. It is also used in compositions for tissue growth or cregeneration. The protein is also used in the treatment of seteoporosis consteoparthritis and in the treatment of periodontal disease and other constearthritis and in the treatment of periodontal disease and other constearthritis and in the treatment of periodontal disease, and consequence is a laboused in the treatment of periodontal disease, and consequence is a laboused in the treatment of periodontal disease, and consequence is a laboused in the treatment of nervous consequence is a laboused for promoting or inversion injury in various calloused as a contraceptives since they exhibit activity or inhibit related activities and as a fertility inducing therapeutic. They are used for conditions coagulation disorders and in treatment and prevention of conditions are contraceptives and in treatment and prevention of conditions are contraceptives and in treatment and prevention of conditions are from conditions and treatment and prevention of conditions are contraceptives and in treatment and prevention of conditions are conditions are conditions and conditions are conditions are conditions are conditions and conditions are conditions are conditions are conditions are conditions are conditions are conditions are conditions are conditions are conditions and conditions are condi
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07-AUG-1998;
25-AUG-1998;
09-SEP-1998;
29-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nutritional sources or supplements. The protein exhibits cytokine, cel proliferation, cell differentiation activities and induces production other cytokines in certain cell populations. The protein also exhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrophobic domains. The DNA sequences can be used as a probe or as a genetic marker. The protein can also be used as a marker, and to identical genetic disorders. The DNA and protein can also be used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human proteins having hydrophobic domains useful for treating osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                             conditions resulting from coagulation activities e.g. myocardial infarction or stroke. They also acts as receptors, receptor ligar inhibitors or agonists of receptor/ligand interactions. They are treat inflammatory conditions such as septic shock, sepsis, ische
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 192-194; 351pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-2000
                                                                                       prevent tumours.
                                                                                                                              reperfusion injury,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes a human protein of the invention, which
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98JP-0224105.
98JP-0238116.
98JP-0254736.
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                                                                                                                          arthritis, and
                                                                                                                              nephritis.
                                                                                                                              They
                                                                                                                                  can
                                                                                                                                                                                                                                                    receptor ligands or
                                                                                                                                  be used
                                                                                                                                                                                                             They are used
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AAV40760/c
ID AAV407
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                                                                                                                                                                                                                                                                                     administered to animals, the protein induces a protective immune (antibody) response against carboxylesterase (CE), so they, or compositions containing CE proteins, are used, therapeutically or as vaccines, to protect particularly mammals and birds, specifically cats and dogs, against haematophagous ectoparasite infestation (HEP), ce specifically fleas. More generally the compositions can be used to treat arthropods generally, including pests of agricultural crops, trees, stored goods etc., also those that are vectors of disease. Fragments of the DNA can be used as probes and primers for identification or production of nucleic acid. Antibodies against the protein can be used for passive immunisation; to screen expression libraries; to isolate the protein and to target cytotoxic compounds to HEP. The compounds containing CE are effective against both adult and larval stages; they
                                                                                                                                                             Matches
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                              AAV40761 standard; cDNA; 1650 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding carboxyl:esterase(s) from fleas - useful, e.g. in vaccines, for preventing infestation by haematophagous ectoparasites, particularly on cats and dogs
                                                                                                                                                                                                                                            Sequence 1650 BP; 542 A; 284 C; 341 G;
                                                                                                                                                                                                                                                                         development, metamorphosis, feeding, digestion and reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence encodes the flea esterase protein, nfE51650 (the complementary strand is shown in AAV40761), of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 188-191; 230pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 felis esterase, nFE51650,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silver GM,
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                            0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wisnewski N;
                                                                                                                                                             0;
                                                                                                                                                                            Score 18; DB 19;
Pred. No. 1.4e+02;
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                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                            482 T; 1 other;
                                                                                                                                                             0;
                                                                                                                                                                                           Length 1650;
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E E X D X A X
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                                                                                                                                                                                                                                                                                                                RESULT
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                               protective immune (antibody) response against carboxylesterase (CE), so they, or compositions containing CE proteins, are used, therapeutically or as vaccines, to protect particularly mammals and birds, specifically cats and dogs, against haematophagous ectoparasite infestation (HEP), specifically fleas. More generally the compositions can be used to treat arthropods generally, including pests of agricultural crops, trees, stored goods etc., also those that are vectors of disease. Fragments of the DNA can be used as probes and primers for identification or production of nucleic acid. Antibodies against the protein can be used for passive immunisation; to screen expression libraries; to isolate the
                                                                            Human vesicular binding protein nucleotide sequence.
                                                                                                                                                                                                 AAV71287;
                                                                                                                                                                                                                                                        AAV71287 standard; DNA; 1723 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein and to target cytotoxic compounds to HEP. The compounds containing CE are effective against both adult and larval stages target CEs, including juvenile hormone, that are involved in development, metamorphosis, feeding, digestion and reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the complementary strand of the DNA encoding the flea esterase protein, nfE51650 (see AAV40760 for coding strand), of the invention. When administered to animals, the protein induces a protective immune (antibody) response against carboxylesterase (CE), so the protein induces a protective immune (antibody) response against carboxylesterase (CE), so the protein immune (antibody) response against carboxylesterase (CE), so the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induced in the protein induce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                      12-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brandt KS, Silver GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematophagous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flea; protective immune response; carboxylesterase; arthropod;
agous ectoparasite infestation; nfE51650; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191-192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542
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1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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VSBP; fibroblast; Aplysia; VAM synaptobrevin binding protein;

Aplysia; VAMP; vesicle associated a ding protein; cancer; inflammation;

membrane protein;

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RESULT 56
AQ67601
ID AAQ676
XX AAQ676
XX 20-NOV
DT 20-NOV
XX Retino
XX Retino
XX Retino
XX PN W09411
XX X
PN W09411
XX X
PD 09-JUI
XX Y
PF 19-NOV
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                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a nucleic acid encoding a purified human vesicle binding protein (designated MVBP). This was obtained by standard cloning and screening procedure, where it was first isolated in incyte clone 148415 from a normal fibroblast library (FIBRNGT01). A comparison of the MVBP with the Aplysia vesicle-associated membrane protein (VAMP)/synaptobrevin binding protein showed that they shared 44% identity. MVBP and its products can be used to diagnose, treat or prevent disorders of cell proliferation (e.g. cancer) or inflammation. Sequences complementary to MVBP can be used to detect MVBP in samples. Abs are used to diagnose conditions associated with MVBP or in assays to monitor patients being treated with MVBP or agonists/antagonists.
                                                                                                                                                                                                                                                                                     Human vesicle binding protein - useful for the diagnosis, treatment and prevention of cell proliferation disorders and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
               19-NOV-1993;
                                                                                                                                                  Retinoblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                              W09412521-A
                                                                                                            Retinoblastoma-associated polypeptide; transcription factor; EF2; cell cycle;
                                                                                                                                                                            20-NOV-1994
                                                                                                                                                                                                   AAQ67601;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1723 BP; 548 A; 356 C; 325 G; 468 T; 26 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-1997;
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                                      09-JUN-1994
                                                                                                                                                                                                                            AAQ67601 standard; cDNA; 1800 BP
                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1999-045229/04
                                                                                     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Fig 1A-D; 58pp; English
                                                                                                                                                                                                                                                                                                                                        l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INCYTE
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                           (first entry)
               93WO-US11310
                                                                                                                                                  protein Ap4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "MVBP"
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                                                                                                                                                                                                                                                                                                                                                   Score 18;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                              RAP; Ap12; ss.
                                                                                                                                                                                                                                                                                                                                                   DB 20;
1.4e+02;
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RESULT
AAF25374
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viral re
                                       WPI; 2001-159529/16.
P-PSDB; AAB31798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA encoding a retinoblastoma (RB) associated protein (RAP), Ap12, was cloned by direct screening of cDNA expression libraries using purified RB protein as probe. Ap12 showed transcription factor E2F and RB binding activities. The 5' and 3' cDNA sequences were determined for Ap2 (AAQ67395, AAQ67596), Ap8 (AAQ67597, AAQ67598) an Ap15 (AAQ67599, AAQ67600), and full-length encoding sequences for Ap (AAQ67601) and Ap10 (AAQ67601), which also encoded RB-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding retinoblastoma-associated polypeptide(s) used for producing prods. for use in studying cell cycling and disregulated cell growth.
                                                                                                                                                            (AVET )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of the Arabidopsis SGS3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2001
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                                                                                                                  Beclin
                                                                                                                                                                                                                                    16-JUL-1999; 99FR-0009417
26-JAN-2000; 2000FR-0001006
                                                                                                                                                                                                                                                                                                                                                      25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                        WO200105951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1800 BP; 747 A; 333
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                                                                                                                                                                                                                                                                                                       13-JUL-2000; 2000WO-FR02052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance;
                                                                                                               C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
18; Conserv
                                                                                                                                                              AVENTIS CROPSCIENCE SA
INST NAT RECH AGRONOMI(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       post-transcriptional
                                                                                                             Elmayan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .92US-0979156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ranscriptional inactivation; RNA degradation; resistance; fatty acid content; protein cont
                                                                                                          Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%;
100.0%;
                                                                                                                                                              AGRONOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "SGS3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                               н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         348 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.4e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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0;

New SGS3 gene from Arabidopsis thaliana, useful for increasing virus

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RESULT S
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Best Local
                                                                                                                                                                                16-DEC-1997;
16-MAY-1997;
20-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1020 aggtgcttgaggaatctc 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous recombination) increases the level of the transgene product. This product may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active,
                                                                                                                     (ASAH )
(NOVO )
(NOVO )
        Production of protein hydrolysate - using protease and releases glycine, useful as flavour improvers in foods
                                                                                             Blinkovsky
                                                                                                                                                                                                                                                      19-NOV-1998
                                                                                                                                                                                                                                                                                W09851163-A2
                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                      Aminopeptidase; protein hydrolysate; glycine releasing; protease; proteinaceous material; flavour; food; baking; animal feed additive; palatability; hydrolysis; solubility; emulsifying; foaming; aroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV82522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance expression
releases glycine, useful 
feed additives
                                                                                                                                                                                                                                15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                      Sphingomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sphingomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV82522 standard; DNA; 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1878 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1;
                                                                                                                                                                      16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                             mouthfeel; crust colour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence encodes the Arabidopsis thaliana SGS3 polypeptide. SGS3 gene is essential for post-transcrintings thatiana SGS3 polypeptide.
                                             1999-045177/04
DB; AAW89587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aggtgcttgaggaatctc 1405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                     ASAHI CHEM IND CO LTD. NOVO NORDISK BIOTECH : NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin or interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in.
                                                                                 Marumotac,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                     capsulata.
                                                                                                                                                                                                                                                                                                                                                                                                                                       capsulata
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plants
                                                                                                                                                                     97US-0069719.
97US-0857886.
97US-0062893.
97DK-0001465.
                                                                                             Brown K,
                                                                                                                                                                                                                                98WO-US09998
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1..1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                575 A; 332 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       mature aminopeptidase I encoding
                                                                                    Mathiansen
                                                                                                                                                                                                                                                                                                      B
                                                                                             Byun T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             when inhibited,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 18;
Pred. No.
                                                                                                                                   INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 554 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                   Fujii M,
TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for increasing transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                              Golightly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
           and
                      enzyme that
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA.
            animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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B

1242

gctggtgtggctggaagc 1259

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γ
                                                           Query Match
Best Local S
Matches 18
                                                                                                                                                                                                  A method has been developed for the production of protein hydrolysates (PH) comprising reacting a protein with: (1) at least one polypeptide with Gly-releasing activity; and (ii) at least one polypeptide with Gly-releasing activity; and (ii) at least one other protease so that the amount of Gly produced is greater than when the protease is used alone. PH are used to improve flavour of foods (e.g. baked goods) and as animal feed additives. PH are preferably also enriched in Glu (free and/or peptide bound), so have improved flavour and palatability. Addition of a polypeptide with Gly-releasing activity increases the degree of hydrolysis (or reduces the amount of enzyme needed) and hydrolysates have better solubility, and emulsifying and foaming properties. Baked goods containing them have improved aroma, mouthfeel and crust colour. The present sequence encodes Sphingomonas capsulata aminopeptidase I, which is used in the method of the invention.
                     2127
                                                                                                                                                                 Sequence 1926 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7;
gctggtgtggctggaagc 2144
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 61; 84pp;
                                                               Conservative
                                                                                                                                                                 362 A; 633 C; 628 G; 303 T; 0 other;
                                                                              0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                             0;
                                                                              Score 18;
Pred. No.
                                                               Mismatches
                                                                              DB 20; 1
1.4e+02;
                                                               0;
                                                                                                    Length 1926;
                                                               Indels
                                                           0;
                                                           Gaps
                                                             0,
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RESULT
AAZ7750
ID AA
09-APR-1998;
                                                   DE19817557-A1
                                                                           Homo sapiens
                                                                                                    gene
                                                                                                               Expressed
                                                                                                                                          Human ovarian
                                                                                                                                                                    10-APR-2000
                                                                                                                                                                                             AAZ77504;
                                                                                                                                                                                                                     AAZ77504 standard; cDNA; 1962
                          21-OCT-1999
                                                                                                                                                                                                                                               59
                                                                                                  therapy;
                                                                                                    sequence tag;
apy; treatment;
                                                                                                                                                                    (first entry)
                                                                                                                                          tumor cDNA library derived EST fragment 55
 98DE-1017557
                                                                                                    EST;
                                                                                                                  human; ovarian tumor; anticancer;
                                                                                                                                                                                                                       ₽Р
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(META-) METAGEN GES GENOMFORSCHUNG MBH.

09-APR-1998;

98DE-1017557

Rosenthal A,

Specht T,

Hinzmann B,

Schmitt

Ą,

Pilarsky

Ç

Dahl

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1999-591920/51 )B; AAY76633, A/

AAY76634,

AAY76635

have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generatic

generation

invention describes novel nucleic acid (cDNA) sequences (A) which

Claim 3;

Page 182-183;

310pp; German.

identification

New nucleic acid sequences expressed in ovarian, tissues, and derived polypeptides, for treatment

and some other, cancer of ovarian cancer and

of therapeutic

agents

specific antibodies. (A) are identified by assembling ESTs (expressed

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RESULT 6
ADV407335/
ID ANV4
XX AV4
XX AV4
AX AV4
XX AV4
XX AV4
XX Este
KW Este
KW Haem
XX Cten
XX W096
XX W96
PT CDS
FT U-1
PR 12-1
XX Brai
DR WPI
DR WPI
DR WPI
DR WPI
PR 12-1
XX P-P:
YX PT e-9
PT ect
XX P-P:
YX PT CDS
TT COS
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CC Thi
CC Com
CC Cand
CC Sto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                            complementary strand is shown in AAV40736), of the invention. When administered to animals, the protein induces a protective immune (antibody) response against carboxylesterase (CE), so they, or compositions containing CE proteins, are used, therapeutically or exactnes, to protect particularly mammals and birds, specifically and dogs, against haematophagous ectoparasite infestation (HEP).
                                                                                                                                                                                          New nucleic acid encoding carboxyl:esterase(s) from fleas - us e.g. in vaccines, for preventing infestation by haematophagous ectoparasites, particularly on cats and dogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence tags) from a particular tissue type before comparison of the expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAZ77450-Z77572 represent the human ovarian tumor cDNA library derived EST fragments described in the method
                                                                                                                                                                                                                                                                      WPI;
               and dogs, against haematophagous ectoparasite infestation (HEP), specifically fleas. More generally the compositions can be used to treat arthropods generally, including pests of agricultural crops, trees,
                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ctenocephalides
                                                                                                                                                              Claim 1; Page 106-109; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                            12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9821324-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Esterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV40735 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention and encode the protein fragments represented
                                                                                                                                                                                                                                                                                                                                 (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haematophagous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1962 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                      1998-297929/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atgaatttcataaaggac 53
                                                                                                                                   sequence encodes the flea esterase protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atgaatttcataaaggac 385
                                                                                                                                                                                                                                                                                                   KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                      AAW57851.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                esterase, nFE51982,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    flea;
                                                                                                                                                                                                                                                                                                   Silver GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          97WO-US20598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protective immune response; carboxylesterase; arthropod; ectoparasite infestation; nfE51982; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31..1520
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    also
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                                                                                                                                                                                                                                                                                                   Wisnewski
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620
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                                                                                                                                                                                                                      from fleas - useful,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                   nfE51982 (the
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                                                       specifically cats
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Best Local
   they, or compositions containing CE proteins, are used, therapeutically or as vaccines, to protect particularly mammals and birds, specifically cats and dogs, against haematophagous ectoparasite infestation (HEP), specifically fleas. More generally the compositions can be used to treat arthropods generally, including pests of agricultural crops, trees, stored goods etc., also those that are vectors of disease. Fragments of the DNA can be used as probes and primers for identification or production of nucleic acid. Antibodies against the protein can be used for passive immunisation; to screen expression libraries; to isolate the protein and to target cytotoxic compounds to HEP. The compounds containing CE are effective against both adult and larval stages; they target CEs, including juvenile hormone, that are involved in development, metamorphosis, feeding, digestion and reproduction.
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                                                                                                                                                                                                           This sequence is the complementary strand of the DNA encoding the fl esterase protein, nfE51982 (see AAV40735 for coding strand), of the invention. When administered to animals, the protein induces a protective immune (antibody) response against carboxylesterase (CE),
                                                                                                                                                                                                                                                                                          Claim
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В QУ

Length 2144;

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This sequence encodes the flea esterase protein, nfE52144 (the complementary strand is shown in AAV40759), of the invention. When CC administered to animals, the protein induces a protective immune CC (antibody) response against carboxylesterase (CE), so they, or CC compositions containing CE proteins, are used, therapeutically or as CC vaccines, to protect particularly mammals and birds, specifically cats CC and dogs, against haematophagous ectoparasite infestation (HEP), CC specifically fleas. More generally the compositions can be used to treat CC arthropods generally, including pests of agricultural crops, trees, CC stored goods etc., also those that are vectors of disease. Fragments of CC the DNA can be used as probes and primers for identification or production of nucleic acid. Antibodies against the protein can be used CC protein and to target cytotoxic compounds to HEP. The compounds CC containing CE are effective against both adult and larval stages; they CC development, metamorphosis, feeding, digestion and reproduction.
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AAV40758/c
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Sequence 2144 BP;

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389 G; 689 T; 1 other;

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AAV40759
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                                                                                                                                          689 A; 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 18;
100.0%; Pred. No.
                                                         0.6%;
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0;
                                                                                                                                                                                             feeding, digestion and reproduction.
                       Score 18;
Pred. No.
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  Mismatches
                                                                                                                                       326 G;
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                         DB 19; 1
. 1.4e+02;
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1.4e+02;
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RESULT 64
RAS96326/C
ID AAZ963
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DT 10-APR
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KW Dacter
XX Treatm
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PR 16-AUG
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XC AAV429
XC O9-NOV
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                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel isolated Streptococcus pneumoniae

polynucleotides (see AAZ95173-Z96494) and their encoded proteins (see

AX85792-Y86182). The DNA, vectors and host cells described in the

method of the invention are useful for the recombinant expression of the

polypeptides. The polypeptides are useful for treatment or prevention of

cuch a polypeptide. They can also be used to screen for compounds which

theract with and inhibit or activate such a polypeptide. The

polypeptides (or DNA encoding them, via gene therapy) are also useful

for inducing an immunological response in a mammal. The antagonists are

useful to inhibit such bacterial polypeptides. The polypeptides are

particularly useful to identify antimicrobial compounds and antibiotics.

They are also useful to determine their role in pathogenesis of

cuch infection, dysfunction and disease.
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                  2765 caagcttgggttgaaaaa 2782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae proteins and related screening compounds for antibacterial activity
                                                        09-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 188-189; 640pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stodola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus
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bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. pneumoniae
                                                                                                           AAV42995;
                                                                                                                                                           AAV42995 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2299 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ96326;
                                                                                                                                                                                                                                                                                       429 CAAGCTTGGGTTGAAAAA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY85980,
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hodgson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prevention; dis
antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY85981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JE,
                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease; diagnosis;
                                                                                                                                                           2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sease; diagnosis; gene therapy; screening;
antibiotic; pathogenesis; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                          score 18; DB; Pred. No. 1.4
                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #154.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 19; 1
1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Τ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            •
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicholas RO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful
                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                          0;
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Streptococcus pneumoniae polypeptide coding region.

24-JUN-1999

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                                                                                                                                                                                                                AAX84399
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                       The polypeptide can potentially be used for the diagnosis and prevention of bacterial infections, especially SP infection. It may be used for the treatment of diseases such as otilis media, conjunctivitis, pneumonia, bacteremia, meningitis, sinusitis, pleural empyema, endocarditis or infection of the cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae polynucleotides - useful for developing products for diagnosis, prevention and treatment of infections pneumonia, bacteremia, meningitis or endocarditis
                     WO9931226-A1
                                            Sphingomonas capsulata
                                                                    peptide sequence cleavage; post-translational processing;
precursor protein activation; ss.
                                                                                         Aminopeptidase; amino acid removal; protein hydrolysate production; hydrolysis; flavour development; enzyme deactivation;
                                                                                                                           S. capsulata IFO12533 aminopeptidase coding sequence
                                                                                                                                                    09-SEP-1999
                                                                                                                                                                             AAX84399;
                                                                                                                                                                                                   AAX84399
                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a Streptococcal polypeptide coding region The polypeptide can potentially be used for the diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 106; 181pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-322654/28
P-PSDB; AAW62719.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       streptococcal; bacteremia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide; ORF; open reading frame; infection; bacterial;
                                                                                                                                                                                                                                                            429 CAAGCTTGGGTTGAAAAA 412
                                                                                                                                                                                                                                                                                                           Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                           66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RH,
                                                                                                                                                                                                   standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                     2299 BP; 585 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (388..1008)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     0.6%;
                                                                                                                                                                                                   3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Knowles
                                                                                                                                                                                                                                                                                                                                                                   514 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                   ₿₽.
                                                                                                                                                                                                                                                                                                                     Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                  491 G; 708 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DJC,
                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prophylaxis;
                                                                                                                                                                                                                                                                                                                     DB 19;
1.4e+02;
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                                                                                                                                                                                                                                                                                                                               Length 2299;
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SSSSSSSS
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AAH51776/c
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Best Local
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                    30-MAR-1999;
30-APR-1999;
10-APR-1999;
14-JUL-1999;
27-JUL-1999;
29-JUL-1999;
29-JUL-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                1911
                                                                                                                                                                                                                                                                                                                                                                                                        2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes the Sphingomonas capsulata IFO12533 aminopeptidase of the invention. The aminopeptidase polypeptides catalyse the removal of amino acids from the "terminal end of peptides", oligopeptides or proteins. They can be used in the production of protein hydrolysates for enhancing the degree of hydrolysis and flavour development, particularly in foods. They can also be used to deactivate enzymes. They can also be used for specific clavage of peptide sequences, e.g. to provide the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1998;
16-DEC-1997;
16-DEC-1997;
                                                                                                                                                                                                                  sbg1; g34665; sbg2; g35017; g35018; chromosome 13q31-q33;
biallelic marker; polymorphism; schizophrenia; bipolar dis
                                                                                                                                                                                                                                                     Chromosome 13q31-q33 biallelic marker containing amplicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blinkovsky /
Marumoto C,
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                      AAH51776 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3000 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Fig
(GEST )
                                                                                                                           30-MAR-2000;
                                                                                                                                                 05-OCT-2000
                                                                                                                                                                        WO200058510-A2
                                                                                                                                                                                                                                                                            29-AUG-2001
                                                                                                                                                                                                                                                                                                   AAH51776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          necessary post-translational processing to activate precursor proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated aminopeptidase polypeptides used in, e.g. food industry
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                                                                                                                                                                                                                                                                                                                                                                                gctggtgtggctggaagc
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DB; AAY22184.
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) NOVO NORDISK BIOTECH INC
) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                              18;
GENSET
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                                                                                                                           2000WO-IB00435
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                            990S-0126903.
990S-0131971.
990S-0132065.
990S-0143928.
990S-0145915.
990S-0146452.
990S-0146453.
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loma A, T
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97DK-0001465.
97US-0069719.
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                      99US-0162288
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lang M;
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Pred. No.
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sorder; ds.
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Sequence.

3001

B₽;

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A;

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C;

533

G;

1011 T;

1 other;

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AAH51601 represents a human genomic nucleotide sequence comprising sbg1, CC 934665, sbg2, 935017 and 935018 nucleic acid sequences located on the CC human chromosome 13931-933 locus. The nucleotide sequences contain CC biallelic markers and polymorphisms. Sequences AAH51602 - AAH51626 and CC PAB62907 - AAB62915 represent cDNA human sbg1 cDNA sequences and protein CC products. AAH51627 - AAH51631 and AAB62916 - AAB62918 represent 935018 CC CDNA sequences and protein products. Primers AAH51362 - AAH51699 are used to isolate sbg1 cDNAs, while sbg1 exons from different primates are CC represented by sequences AAH51642 - AAH51699. Nucleotide sequences of CC amplicons which comprise biallelic markers located on the chromosome CC 13931-933 locus are represented in AAH51819. Nucleotide sequences of CC are represented in the sequences by degenerate/undefined base codes. PCR primers AAH51818 and AAH51819 are used in the isolation of sequences of the invention. The biallelic marker containing nucleotide sequences are used to determine the identity of the nucleotide at a biallelic marker in a sample DNA sequence. The nucleotide sequences may be labelled and used for genotyping by determining the identity of a nucleotide at a Region CC subjects. By determining the frequency of a biallelic marker in a biological sample from single or multiple consultation an association between a genotype and a trait a banlotype and
                                                                    population an association between a genotype and a trait, a haplotype and a trait and a phenotype and a trait can be detected. The sequences can be used to determine a predisoposition to or early onset of schizophrenia or bipolar disorder or a beneficial response to or side effects related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotides comprising sequences from sbg1 markers are used for genotyping and detecting s disorder and predisposition to these disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
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                                                   treatment against schizophrenia or bipolar disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 680-681; 737pp; English.
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schizophrenia or bipolar
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RESULT 6
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Best Local Similarity
Matches 18; Conserv
30-MAR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                     sbg1; g34665; sbg2; g35017; g35018; chromosome 13g31-g33; haplotype; biallelic marker; polymorphism; schizophrenia; bipolar disorder; ds.
                                                                                                                                                  Chromosome 13q31-q33 biallelic marker containing amplicon
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                                       30-MAR-2000;
                                                                              WO200058510-A2
                                                                                                 Homo sapiens
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                                                                                                                                                                                          AAH51787;
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                                                                                                                                                                                                                                 68
                                                                                                                                                                                                             standard; DNA; 3001
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                                       2000WO-IB00435
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99US-0126903.
99US-0131971.
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Pred. No.
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1.4e+02;
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RESULT (
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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27-JUL-1999;
29-JUL-1999;
29-JUL-1999;
29-JUL-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       population an association between a genotype and a trait, a haplotype and a trait and a phenotype and a trait can be detected. The sequences can be used to determine a predisoposition to or early onset of schizophrenia or bipolar disorder or a beneficial response to or side effects related to treatment against schizophrenia or bipolar disorder.
                                                                                                            SGS3
                                                                                                                                                                                                                                                                                                                                          AAH51601 represents a human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cohen D,
Essioux L;
                                                                                                                                            Genomic sequence of the Arabidopsis SGS3 gene
                                                                                                                                                                                                                     AAF25373;
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   exon
                                                      Arabidopsis thaliana
                                                                                           viral
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                                                                                                                                                                                                                                                                                          69
                                                                                     gene; post-transcriptional inactivation;
l resistance; resistance; fatty acid conta
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                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3001 BP;
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99US-0145915.
99US-0146452.
99US-0146453.
99US-0162288.
 Location/Qualifiers 696..1658
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                                                                                       tion; RNA content;
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                  Human colon cancer cell line Km12L4-A cDNA library derived seq#1078
                                                    27-JUL-2001 (first entry)
                                                                                         AAH31144;
                                                                                                                             AAH31144
                                                                                                                                                                                                                                                                                                                                                                                Sequence
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26-JAN-2000; 2000FR-0001006
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INST NAT RECH AGRONC
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                                                                                                                                                                                                                                                                                          Conservative
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2739..2949
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                                                                                                                                                                                                                                                                                                                                                                                956 A; 561 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and,
                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2379
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                                                                                                                                                                                                                                                                                                                             0.6%;
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                                                                                                                                                                                                                                                                                                         Score 18;
Pred. No.
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rne present sequence represents the genomic sequence of the Arabidopsis thaliana SGS3 gene. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous recombination) increases the level of the transgene product. This product may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. an immunoglobulin or interferon.
DB 22,
3. 1.4e+02;
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                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    Matches
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Reinhard C, Giese K, R
Lamson G, Drmanac R, C
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28-SEP-1998;
29-SEP-1998;
08-OCT-1998;
27-OCT-1998;
   Kidney injury
                                                                                                                                                                                                                  3465 aaagaaccctctgaaaaa 3482
                                                                                                                                                                                                                                   2831 aaagaaccctctgaaaaa 2848
                                                                  01-MAR-1999
                                                                                                   AAV80604;
                                                                                                                                AAV80604 standard; cDNA; 3942
                                                                                                                                                                                                                                                                                                                                                                   Sequence 3529 BP; 1248 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide library the form of an array to
                                Kidney injury associated molecule HW050 cDNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 501-502;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; diagnosis; colon cancer; cancer; mallgnant; chromosome mapping; detection; colon cancer cell line Kml2L4-A; ss.
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                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                    Conservative
                                                                (first entry)
associated molecule; kidney injury related molecule;
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98US-0102180.
98US-0102380.
98US-0103815.
98US-0105877.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising 1079 defined sequences, useful o detect cancer or susceptibility to cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Innis MA, Garcia PD, Sudduth-Klinger J;
Randazzo F, Kennedy GC, Pot D, Kassam A;
Crkvenjakov R, Dickson M, Drmanac S, Labat
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502pp; English.
                                                                                                                                                                                                                                                                                                                                                                   778 C;
                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                 ВР
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                                                                                                                                                                                                                                                                                                                                                                 692 G; 803 T;
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1.5e+02;
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                                                                                                                                                                                                                                                                                                                Length 3529;
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CC (KIM) CDNA COINCE KIM Proteins can be administered therapeutically collections. Kim proteins can be administered therapeutically collections of damaged tissue (e.g. renal tissue), since the KIM proteins care upregulated in injured or regenerating (especially renal) tissues. CC KIM fusion proteins, conjugates, antibodies and vectors can also be used therapeutically, e.g. these or the KIM proteins may be included with an acceptable carrier in pharmaceutical compositions, useful for therapy/ CC prophylaxis of conditions associated with disfunction/disregulation of CC KIM genes or proteins, especially renal diseases or impairments of renal CC function in humans (e.g. acute renal failure, acute nephritis). The CC polynucleotides can be used to produce antisense sequences which, when CC internalised into cells, can disrupt expression of a cellular KIM gene, CC also useful in therapy (e.g. to block the growth of tumours dependent on CC KIM for growth) or compositions. The proteins and polynucleotides are CC (indicative of increased risk, or presence of, renal injury/diseases (indicative of increased risk, or presence of, renal injury (indicative of increased risk, or presence of, an autoimmune response or abnormal cc also be used to locate KIM-producing cells (especially specific loci, e.g. issue masses abnormal transported tissue). The proteins can cc also be used to locate KIM-producing cells (especially specific loci, e.g. of issue masses abnormal transported to the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-045312/04
P-PSDB; AAW86320.
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23-MAY-1997;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9853071-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence represents a kidney injury associated molecule
                                                                                     tissue masses abnormally producing/expressing KIM such as tumours ing from/affecting renal tissue), by contacting cells with an eable KIM-binding reagent and imaging reagent accumulation.
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3942 BP;
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97US-0047490
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complement (3542..3733)
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908 A; 1019
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C; 1087 G; 928
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В

Matches

**Local** 

l Similarity 18; Conser

Conservative

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100.0%; 0.6%;

Score 18; Pred. No.

DB 20; 1.5e+02;

Length 3942;

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AAA64473/c
ID AAA64473 standard; DNA; 3969 BP
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784.898
/*tag= f
/number= 2
899.1015
/*tag= g
/number= 3
1016.1087
/*tag= h
/number= 3
1088.1119
/*tag= i
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/*tag= d

/number= 1

735..783
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535..652
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2182..2257

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                                                                                /*tag= q
/number= 8
2000..2081
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/number= 7
1940..1999
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163:1723
/*tag= n
1724..1866
/*tag= o
/number= 7
1867..1939
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517..518
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          Novel polynucleotide encoding astaxanthin synthase useful for producing recombinant cells for producing astaxanthin from beta-carotene
                                                      WPI; 2000-559874/52.
P-PSDB; AAB08713.
                                                                                                                                                       09-MAR-1999; 99EP-0104668
01-FEB-2000; 2000EP-0101666.
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2963.3050
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3051.3113
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3114.3171
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3248.3321
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3424.331
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3514.3700
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2543.2618

/*tag= x

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/number= 12
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03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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25-APR-2000;
09-JUL-2000;
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                     Claim 1;
                                                                            WPI; 2001-442253/47.
P-PSDB; AAM39259.
                                                                                                                                 Tang
                                                                                                                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
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                                                                                                                                                                                                                                                                              26-DEC-2000;
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                                                      Novel
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                                                                                                                                                                                                                                                                                                                                                                                chemokinetic;
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                                         nucleic acids and as central nervous
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18; Conserv
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Wang
                    SEQ
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                                                                                                            Zhou P,
                                                                                                                                                                            2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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                     ID NO
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2000US-0552317.
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Wehrman T, X
Goodrich R,
                    618;
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                   10078pp; English.
                                         polypeptides, useful system injuries -
                                                                                                         Chen R, Ma Y,
, Xu C, Xue AJ,
R, Drmanac RT;
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hes 0;
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                                                                                                                    Qian XB,
Yang Y,
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                                                    treating
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Zhang
                                                    disorders
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human nucleic acids (AAI57798-AAI61369) and

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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central netrous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activiny, Chemotactic/Chemokinetic activity, hamostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                              Wang
                                                                                         Tang
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                                  P-PSDB;
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                                                                                                                                                                                                                                                                                                                               chemokinetic;
leukaemia; ss
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                                                                     Zhao
                                                                                                               (HYSE-)
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                                                                                                                                                                                                                                                               26-JUL-2001.
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                                                                                                                                                19-OCT-2000;
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 l nucleic acids as central nerv
                                                                   YT,
                                             2001-442253/47
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18; Conser
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                                                                                                               HYSEQ INC.
                                                                   Liu C
Wang z
Zhou
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2000US-0553317.
2000US-05598042.
2000US-0620312.
2000US-0653450.
2000US-0663450.
2000US-0693036.
2000US-0727344.
                                                                u C,
1 Z,
u P,
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                                                                                                                                                                                                                                                                                                                                          thrombolytic; drug screening;
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 cids and nervous
                                                                              Asundi V,
                                                                    Wehrman T,
Goodrich
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polypeptides, useful system injuries -
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Xu C,
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           for treating
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            disorders
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Claim 1;

SEQ ID NO 4190; 10078pp; English.

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Matches 18
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06-MAY-1997;
16-MAY-1997;
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A computer readable medium has been developed which has recorded 982 nucleotide sequences isolated from the Enterococcus faecalis AAX12938 to AAX13919 represent these nucleotide sequences which a
                                                                                                  New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
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3258 aaagaaccctctgaaaaa 3275
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Note: The sequence data for this patent did specification.
                                                        Claim 1; Page 1248-1251; 2084pp; English.
                                                                                                                                                                                              Barash
                                                                                                                                                                                                                                                                                                                                                                               WO9850555-A2
                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus
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vaccine; attenuation; computer
                                                                                                                                                                 WPI; 1999-045171/04.
                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                    04-MAY-1998;
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                                                                                         infection
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                                                                                                                                                                                             SC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  faecalis genome contig SEQ ID NO:261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                       97US-0066009.
97US-0044031.
97US-0046655.
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100.08; F1
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Pred. No.
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readable medium; ds.
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primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
Sequence 4951 BP; 1563 A; 981 C; 735 G; 1665 T; 7 other;
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2527 gcttgtctgcaaatgcag
                       18;
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Other GSSs: CITB1-E1-2528J13.TR
Other GSSs: CITB1-E1-2528J13.TR
Contact: Shaying Zhao, William Nierman, Ma
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 208
Tel: 301 838 0208
Fax: 301 838 0208
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Clones are availabe from Research
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/clone="2528J13"
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                                                                                                                                                      Unpublished (2000)
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Hi-Tech Park,
                                                                                                                                                                                                    Qian,B., Wu,T., Huang,Q., Huang,C., Xu,X., Li,N., Peng,Y., Liu,F., Qu,Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Y., Gu,Y., Chen,Z. and Han,Z.
                                                                                                                                                                                                                                                                                                                      AV719179
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EST.
                                                                                        Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
                                                                                                                          351 Guo Shoujing Road, Zha
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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1 (bases 1 to 480)
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/clone_lib="GLC"
/tissue_type="corresponding non
/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
/clone="GLCEQA10"
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Ren,S., Zhong,M., Lu,G.,
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mRNA sequence. 16-OCT-2000

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Pudong,

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Xu, Z.,

Xiao, H. Yang

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qx57b01.x1 NCI_CGAP_Pan1
mRNA sequence.
AI263294
       DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 364.
Location/Qualifiers
                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 364)
                                                                                                                                               Unpublished (1997)
                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
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                                      Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 1
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 371)
                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                          EST.
            Email: hanzg@chgc.sh.cn
This clone is available at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE: 2005417"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
Location/Qualifiers
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                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@nail.nih.gov
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Li
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                       found through the I.M.A.G.E. Consortiu www-bio.llnl.gov/bbrp/image/image.html Seq primer: -40UP from Gibco
                                                             Genome Sequencing Center Clone distribution Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AW337918
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he12h11.x1 NCI_CGAP_CML1
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                                                                                                                                                                                   Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy
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quality sequence stop: 201
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/db_xref="taxon:9606"
/clone="GLCEQA10"
/clone_lib="GLC"
/clsue_type="corresponding non ca
/dev_stage="Adult"
/lab_host="SOLR"
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RST29913 Athersys RAGE Library
BG210375
BG210375.1 GI:13732062
                                                                                                                                                                                                            Athersys, Inc.
3201 Carnegie
                                                                                                                                                                                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                                        Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001)
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/clone_lib="NCI_CGAP_CMLI"
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/lab_host="DH10B"
/note="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies."
86 a 54 c 38 g 83 t
                                                                                       Location/Qualifiers
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/organism="Homo sapiens
/clone_lib="Athersys RAGE Library"
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                                                                                                                                                                                                             Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, Use of human BAC End Sequences for Sequence-Ready Map Building
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RPCI11-93C9
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

107 g 149 t 1 others
                    /db_xref="taxon:9606"
/clone="RPCI-11-93C9"
/clone_lib="RPCI-11"
                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="See 'Creation of Genome-wide Protein Expression
/sex="Male"
                                                                               /db_xref="GDB:7535384"
                                                                                                                               1. .553
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="HT1080"
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.TV RPCI-11
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99.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 172; DB 11;
Pred. No. 2.1e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
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genomic clone
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RESULT 8
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                    BASE COUNT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2650 tcgacaggatgaacgtgctagaacagctcaccgcactgatgctgccctgggggctgtgacg
                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2710 tgcaaggcagcctgagcagcctgttgaaacatttggaggaggtcccacaactcgtcaagc 2769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGGTTGAAAAACTGGAGACTCACAGATACAGAGATTAGAATTTTAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt TCGACAGGATGAACGTGCTAGAACAGCTCACCGCACTGATGCTGCCCTGGGGGCTGTGACG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Seg primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae, 1 (bases 1 to 509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW418826
AW418826.1 GI:6946758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW418826 509 bp mRNA EST ha21e11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170
                    161
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                    മ
                                 purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
RPCIII Human Male BAC Library"
a 107 c 114 g 162 t
                                                                                                                                                               /notce"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP
                                                                                                                                                                                                                                                     /clone="IMAGE:2874380"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                         1. .509
                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project (CGAP),
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                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.2%; Score 162; DB 10; Best Local Similarity 100.0%; Pred. No. 2.3e-70; Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
           2384 agctgaaggcctgaaaaacctgaagaagatgtgtttatttcatttgacccacttgtctga 2443
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                                                                   Local Similarity
AGCTGAAGGCCTGAAAAACCTGAAGAAGATGTGTTTATTTCATTTGACCCACTTGTCTGA 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                             Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ112439 630
CIT-HSP-2372C1.TR
                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                      end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Other_GSSs: CIT-HSP-2372C1.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                                              primer: M13 Reverse
ss: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                       Institute for Genomic Research
Medical Center Dr., Rockville,
                                                                                                                                          188
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301 838 0208
                                                        Conservative
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                                                                                                                                          HindIII"
a 126 (
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2372C1"
                                                                                                                                                                                                                                                                     1. .630
                                                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                             /clone_lib="CIT-HSP"
                                                                   4.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:3484599
                                                                                                                                          O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIT-HSP
                                                        0,
                                                                   Score 146; DB 13;
Pred. No. 2.9e-62;
                                                                                                                                       124 g
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                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence Database for Sequence-Ready
                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens genomic clone 2372C1, DNA
                                                                                                                                                                                                                                                                                                                                                                                                       MD 20850, USA
                                                      0;
                                                                               Length 630;
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                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 942
High quality sequence stops: 347
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 942
Std Error: 0.00
Seg primer: M13RP1
Seg primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST project Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H25984 412 bp mRNA EST 10-JUL
y156g07.rl Soares breast 3NbHBst Homo sapiens cDNA clone
IMAGE:162300 5', mRNA sequence.
Similarity 100.
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 347 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University Scho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                       Bonaldo."
a 84 c
                                                                                                                                                                                                                          double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot =
                                                                                                                                      20. Library constructed by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:162300"
                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Soares breast 3NbHBst"
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:576544"
                                                                                                                                                                                                                                                                                                                                    /sex="Female"
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                  4.0%;
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   0;
Score 124; DB 11;
Pred. No. 3.7e-51;
0; Mismatches 0;
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tggtgtggctggaagcctcagtttggtcctcagcacctgtaagaac 2174
                                                   ATATCTGGGGAAAATATTCAGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTA 217
                                                                                                                       106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ624020 470 bp
HS_5378_B2_C12_SP6E RPC
genomic clone Plate=954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 470.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clones are derived from the human BAC library RPCI-11. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           scanning the human genome
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                             142
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206) 616-3618
(206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jwallace@u.washington.edu
                                                                                                                                                                                                                                       /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI Male blood DNA was isolated from one randomly chosen and partially digested with a combination of EcoRI ar EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=954 Col=24 Row=F"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                                                                                                           /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                     3.4%;
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                                                                                                                     Score 106; DB
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Col=24 Row=F, I
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. 4.6e-42;
ches 0;
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                                                                                                                   Gaps
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/db_xref="taxon:9606"
/clone="IMAGE:1655717"
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IMAGE:4082074 5',
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Researc
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81; Conser
                                                                                  Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: pDNR-LIB (ggccattatggcc);
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/clone_lib="NIH_MGC_53"
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/db_xref="taxon:9606"
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100.0%; Pred. No.
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Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 635)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B58691 635 bp DNA CIT-HSP-2013L21.TF CIT-HSP
                                                                                                       Class: BAC ends
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                                                                                                                                                                  end search page:
                                                                                                                                                                                         Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                  Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                            9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                          Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                Other_GSSs: CIT-HSP-2013L21.TR
                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a random BAC End Sequence Database for Sequence-Ready Map
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Clones are derived from the human BAC library RPCI-11.
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Tel: 301 838 0200
Fax: 301 838 0208
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
45 c 46 g 59 t
/db_xref="GDB:7042463"
/db_xref="taxon:9606"
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/clone="RPCI-11-78E13"
/clone_lib="RPCI-11"
                                         /organism="Homo sapiens"
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/db_xref="GDB:7529676"
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                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                      Soares and M. Fatima Bonaldo.
95 c 86 g 137 t
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/lab_host="DH10B"
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/clone_lib="CIT-HSP"
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RESULT 18
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                                   AQ8893169 404 bp DNA GSS
HS_2161_B1_A01_T7C CIT Approved Human Genomic sapiens genomic clone Plate=2161 Col=1 Row=B, AQ889169
                                                                                                                                                                                                                                                                                              30;
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High quality sequence stop: 96.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0180-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto, E.,
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Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Adult"
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E., García Correa, R., Verjovski-Almeida, S.,
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                      GI:6345359
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RESULT 19
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Best Local Similarity
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AQ497022
AQ497022.1
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Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2161 row: B column: 1
Seq primer: T7
                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 4.3)
                                                                                                                                                                                                                                                                                                                                              AQ497022 443 bp DNA GSS 28-APK-1999 HS_5197_B1_C11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=773 Col=21 Row=F, DNA sequence.
401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                               Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                  Mahairas, G.G., Wallace, J.C., Keller, A., Shaker, R., Furlong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
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Location/Qualifiers
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Fax: (206) 616-3887
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 404)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
                                                                                                   99380589
                                                                                                                                 scanning the human
                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping
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                                                                                                              ng the human genome Natl. Acad. Sci. U.
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E-Coli DH10B"
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/clone="Plate=2161 Col=1
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                                                                                                                 U. S. A.
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g,J., Young,J., Zhao,S., Adams,M.D.
                             Seattle, WA 98109, USA
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Adams,M.D.
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RESULT 20
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                                                                                             Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                   Contact: Shaying Zhao, William Nierman, Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contract Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                              Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                  Other_GSSs: RPCI-11-343A21.TV
                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
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RPCI-11-343A21.TJ
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Location/Qualifiers
                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                           Use of BAC End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao, S., Adams, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                Email:
                                                                                                                                                                                                                                                                                                                                                                           Map Building
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1 (bases 1 to 674)
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                                      BAC ends
                                                                                                                                                                                              hbe@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI
Male blood DNA was isolated from one randomly chosen
and partially digested with a combination of EcoRI an
EcoRI Methylase. Size selected DNA was cloned into th
pBACe3.6 vector at EcoRI sites"

90 c 75 g 129 t 1 others
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/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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DEFINITION ACCESSION
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                                                                                                                                                                                                                                                                               source
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MR3-HN0052-261200-002-c12 HN0
BF829853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF829853.1
                                                                                                                                                                                                                                                                                                                                                                                       Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR3&t2=MR3-HN0052-261200-002-c12&t3=2000-12-26&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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+55-11-2707001
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 138 c 133 g 185 t
                                                                               /note="Organ: head_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GDB:7631348"
/db_xref="taxon:9606"
/clone="RPCI-11-343A21"
/clone_lib="RPCI-11"
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                                                             tissue mRNA and cDNA amplification were performed
                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone_lib="HN0052"
                                                                                                                                                                                              /dev_stage="Adult"
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus
AV268403
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Automated filtration-based high-throughput plasmid
System. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazak, Y., Ozawa, T., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazak, Y., Ozawa, Y., Muramatsu, M., Okazak, Y., Ozawa, Y., Muramatsu, M., Okazak, Y., Ozawa, Y., Muramatsu, M., Okazak, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., Ozawa, Y., O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Taawa,M., Watahiki,M., Ozawa,
Matsuura,S., Carninci,P., Muramatsu,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (R 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site (http://genome.rtc.riken.go.jp) for
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                                     /tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="4930534P12"
                                                                                                                                                                                                    (вотна)
                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus'
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/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                              /sex≖"male"
                                                                                                                                                                                                                                     /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.7%;
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4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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Hayashizaki
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BASE COUNT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                              Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-103A13.TJB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao,S., Nierman,W., Malek,J., Shatsman,S., Al
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A.,
Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ740007 437 bp DNA GSS 25-JAN-2001
RPCI-24-103A13.TV RPCI-24 Mus musculus genomic clone RPCI-24-103A13
                                                                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGACCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_
/note="Vector: pTARBAC1; Site_1: BamH1; Site_
RPCI-24 Mouse BAC Library produced by Pieter
                                                                                               /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-103A13"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                            /sex="Male"
                                                                                                                                                                                             /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                              row: A column: 13
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6 c 31 g
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    Site_2:
Pieter de
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  BamH1;
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VERSION KEYWORDS

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Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 26 row: D column: 1 Seq primer: T7 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: RPCI-23-26D1.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao,S., Nierman,W., Feldblyum,T., Malek,J.,
B., Levins,M., Mcgann,S., Tsegaye,G., Geer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nouse mouse
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                                                                                         /note-*organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). " a 32 c 21 g 53 t
                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="RPCI-23-26D1"
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                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                /sex="Female"
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100.0%;
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40;
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                  Length 163;
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Murinae; Mus.

Dubuque, T.,

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AA784099 CECCUCA
                                                                                                vs68a01.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
IMAGE:1151400 5', mRNA sequence.
AA821339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Advanced Center for Genome Technology,
620 Parrington Oval, Norman, OK 73019,
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Bruce A. Roe, University of Oklahoma, Department of Chemistry and Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella nidulans
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
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                  Mus musculus
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Prade,R. and Roe,B.
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                                       house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dLxref="taxon:162425"
/dDxref="taxon:162425"
/clone="fd1g08al"
/clone="fd1g08al"
/clone="b="Aspergillus nidulans 24hr asexual
/clone="b="Aspergillus nidulans 24hr asexual
/clone="b="Aspergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="Vector: pBlueScript Sr; Site_1: Site_2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript
3' end of cDNA cloned into XhoI site of pBlueScript"
a 94 c 75 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Emericella nidulans"
/strain="FGSC A26"
                                                                                 GI:2891207
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                                                                           Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 371)

1 (Dases 1 to 371)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                        A1645009 371 bp mRNA EST 29-API vs68a01.y1 Stratagene mouse skin (#937313) Mus musculus IMAGE:1151400 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,
                Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                          The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                             house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 343)
Washington University School of Medicine
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/dev_stage="l1 weeks old"
/lab_host="SoLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
/ Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1151400"
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Pred. No.
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RESULT 28
AZ223093/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (lnfo@resgen.com). BAC end page:
                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                    Unpublished (1999)
Other_GSSs: RPCI-23-94H20.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ223093 432 bp DNA GSS 14-JUN-2000 RPCI-23-94H20.TV RPCI-23 Mus musculus genomic clone RPCI-23-94H20.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                                                                                                                                                                                                                                                                         Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                 and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Nierman,W., Feldblyum,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence.
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                Levins, M., Mcgann, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
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/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI
/site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Whole skin from 11 week old C57BL/6 fenale mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
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/clone="IMAGE:1151400"
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/strain="C57BL/6"
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Rodentia;
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Pred. No.
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. 41;
                                                                                                                                                                                                                                                                                                                                                                         Malek, J.,
                                                                                                                                                                            MD 20850, USA
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FEATURES
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                                                                                                                                                                 High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ555443 437 bp DNA HS_5224_A2_B05_SF6E RPCI-11 Human Male genomic clone Plate-800 Col=10 Row-C, D AQ555443 GI:4914996
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      Class: BAC ends
High quality sequence stop: 437
Location/Qualifiers
                                                                           Seq primer: SP6
                                                                                              http://www.htsc.washington.edu
Plate: 800 row: C column: 10
                                                                                                                                BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                             99380589
                                                                                                                                                                                                                                                                                                                                                                                                                scanning the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 437)
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ss: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
a 123 c 122 g 112 t
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/strain="C57BL/6J"
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/clone="RPCI-23-94H20"
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                                                                                                                                         Local Similarity 100 nes 21; Conservative
            AZ360053 602 bp DNA GSS 02-OCT-2000 1M0103H11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0103H11 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS00SV2 462 bp DNA GSS 28-JUN-1999 Arabidopsis thaliana genome survey sequence SP6 end of BAC T2N9 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope.
Direct Submission
AZ360053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salanoubat, M., Choisne, N., Artiguenave, F., Brottier Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      survey sequence.
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60 c 81 g 128 t
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Male blood DNA was isolated from one randomly chosen donor
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/clone="Plate=800 Col=10 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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87 c 70 g
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/clone_lib="TAMU"
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/strain="Columbia"
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                 602592168F1 NIH_MGC_79 Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 602
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0103 row: H column: 11
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Fax: 801 585 7177
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mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
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                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pubmit ends in the vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector NNA and traperformed into
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                                                                                                                                                                                                                                                                                                                                                          adaptored vector DNA, and transformed into chemically-competent E. coli XI10-Gold (Stratagene) cells and selected for ampicillin resistance."

153 c 139 g 171 t
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory Mouse DNA Resource
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/sex="Male"
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/clone="UUGC1M0103H11"
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/strain="C57BL/6J"
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                                                                          Genes expressed in molting L3
Unpublished (1997)
Contact: Steven A. Williams
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1 (bases 1 to 1147)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                   Molecular Parasitology
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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Tissue Procurement: CLONTECH Laboratories, Inc.
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Contact: Robert Strausberg, Ph.D.
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BG571228.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Site_1: Sfil (gyccqctcggcc); Site_2: Sfil (gyccattatggcc);
S' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.3 kb (range 0.5-4.0 kb): 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
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/db_xref="taxon:9606"
/clone="IMAGE:4719424"
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/lab_host="DH10B (T1 phage-resistant)"
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Department of Biological Sciences
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                                                                                                                                                                             Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
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BE638399
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SWOVL2CAS15B03SK Onchocerca volvulus L2
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                                                                    Email: genome@smith.edu
Seq primer: pBluescript SK.
                                                                                                                                     Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                           Genes expressed in L2 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams, S.A.
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1 (bases 1 to 73)
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/lab_host="XLI-Blue MFF'"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library was constructed by Sara Lustigman and Michelle Lizotte Waniewski in the Laboratory of Dr. S. A. Williams The library is available from Dr. Sara Lustigman (email: slustigmenybc.org)."

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                                    Location/Qualifiers
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/db_xref="taxon:6282"
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5B03SK Onchocerca volvulus L2 larvae cDNA (SAW98MLW-OvL2)
volvulus cDNA clone SWOvL2CAS15B03 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         volvulus
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hes 0;
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HS_2255_B2_H03_MR CIT Approved Human Genomic Sperm Library
Sapiens genomic clone Plate=2255 Col=6 Row=P, DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seati Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 205)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keller, A., Shaker, R., Furlong, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                             High
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                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC,
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double-stranded CDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 7.3 x 1024 independent recombinants and the average insert size is approximately lkb.The library was constructed by Michelle Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and
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/db_xref="taxon:6282"
/clone="SWOVL2CAS15B03"
/clone_lib="Onchocerca volvulus L2 larvae
                  E-Coli DHIOB"
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/note="Vector: Lambda Uni-ZAP XR;
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                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC
                                                                        /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                              /clone="Plate=2255 Col=6
                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available
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BI315256
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
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African clawed frog.
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Seq primer: -40RP from Gibco
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human.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B (phage-resistant)"
/note-"0rgan: whole embryo; Vector: pcMV-spORT6; Site_1:
Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 2:1 kb. Constructed by Life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Xenopus laevis"
/db_xref="taxon:8355"
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9; Mismatches
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                                                                                                                                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACATCACATCTGTAACAA 111
                                                                                                           Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
                                                                                                                                                                                                     Onchocerciae; Onchocerca.

1 (bases 1 to 225)
Williams,S.A., Lizotte-Waniewski,M.,
Genes expressed in molting L3 larvae
                                                         Fax: 4135853786
                                                                           College, Northampton, Tel: 4135853826
                                                                                                                                                                                                                                                                           Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
AI366637
                                                                                                                                                                                                                                                                                                                                                                                                                       AI366637 225 bp mRNA EST 08-JAN-1999 SWOV3MCAM11C04SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM11C04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 216)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                               Onchocerca volvulus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
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il: genome@smith.edu
primer: pBluescript SK.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

a 65 c 37 g 57 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Thy1"
/tissue_type="thyroid"
/lab_host="DH10B"
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/clone="IMAGE:943135"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                             MA, 01063, USA
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AI603832
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A1603832
                                                                                                                                                                                       Fax: 4135853786
                                                                                                                                                                                                           Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                       Onchocercidae;
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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2364 gaagaagatgctataaaact 2383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWOV3MCAM27A08SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM27A08 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes expressed in molting L3 Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: pBluescript SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome@smith.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Onchocerca volvulus.
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a 39 c 57 g 64 t
/clone="SWOv3MCAM27A08"
/clone_lib="Onchocerca volvulus molting
(SL96MLW-OvmL3)"
                                                                                                                                             /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                  /organism="Onchocerca volvulus"
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/db_xref="taxon:6282"
/clone="SWOy3MCAM11C04"
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; Pred. No. 1.3e+02;
0; Mismatches 0;
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DEFINITION
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                                                                                                                           source
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                                                                                                                                                                                  Email: Szhao@tigr.org

Email: Szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Clones are darived from the mouse BAC library RPCI-24. For BAC

Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 180 row: D column: 14

Seq primer: SP6

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999) Other_GSSs: RPCI-24-180D14.TV
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RPCI-24-180D14.TJ RPCI-24 Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Nierman, W., Malek, J., Shatsman, S., Al
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A.,
Russell, D., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
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//lab_host="XL1-Blue MRF/"
//lab_host="XL1-Blue MRF/"
//note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
//note="Vector: Lambda Uni-ZAP XR; Site_1: Fhird-stage
larvae, L3, were isolated from infected black flies in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNAse H
and name and the larvae (mR) are constructed in the Name A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has I x 10E6 independed recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigmanybc.org)."
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-180D14"
                                                                                                                                                        Location/Qualifiers
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100.0%; Pred. No.
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1.3e+02;
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VERSION KEYWORDS

ACCESSION

SOURCE

ORGANISM

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AUTHORS

COMMENT

JOURNAL

FEATURES

Query Match Best Local Similarity

0.6%;

Score 20; Pred. No.

DB 10; . 1.3e+02;

RESULT 4 AZ891870

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BASE COUNT ORIGIN

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RESULT 41
AW357412
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20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                     Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 20 row: J column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                        and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Haaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases
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         /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: xhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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/cell_type="Spleen/Brain"
/cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
nvx "
                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                                                                                                                                     /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                              Location/Qualifiers
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Pred. No. 1.3e+02;
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RESULT 43
AA670222/c
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Other GSSs: Sheared DNA-48N4.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MI
Tel: 301 838 0208
Fax: 301 838 0208
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Determination of clone end sequences from Trypanosoma 10.1 sheared DNA library
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Sheared DNA-48N4.TR Sheared DNA
Sheared DNA-48N4, DNA sequence.
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1 (bases 1 to 336)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pUC18; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical propagation and was a project of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the con
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/strain="TREU927/4 GUTat 10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Approach, eds. M. Vaudin and B. Barell, Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="Sheared DNA-48N4"
/clone_lib="Sheared DNA"
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                                                                                                                                                                                                                                                                                           0.6%; Score 20; DB 13; 100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 g
                                                                                                                                                                                                                                                            Mismatches
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RESULT 4
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JOURNAL
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Best Local Similarity
                                          AUTHORS
                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                        137 CTCAGCAGGGCCCAGGGTGG 118
                                                                                                                                                                                                                                                                                                                                          648 ctcagcagggcccagggtgg 667
                                Mammalia; Eutheria; Rodentia; S
1 (bases 1 to 380)
Dunn, D., Aoyagi, A., Barber, M.,
                                                                                                                                                                                          AZ991565 380 bp DNA GSS 27-APR-2001
2M0275B24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone_UUGC2M0275B24 R, DNA sequence.
                                                                                                                                            GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
   Islam,H., Longacre,S., Mahmoud,
,M., Rose,M., Rose,R., Stokes,F
                                                                         Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                      Mus musculus
                                                                                                                                                              AZ991565.1 GI:13862792
                                                                                                                                                                                 AZ991565
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White,Y., Wylie,T., WaterstowashU-NCI human EST Project Unpublished (1997)
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                                                                                                                          house mouse.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="15 wk post natal"
/lab_host="DH10B"
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/clone="IMAGE:878757"
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                                                                     Chordata;
Rodentia;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 20; pred. No.
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                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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 Beacorn,T., Duval,B., Hamil,C.,
,M., Meenen,E., Pedersen,T., Rei
R., Tingey,A., von Niederhausern
                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; I
1.3e+02;
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Pedersen,T., Relli
von Niederhausern,A
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Best Local (
   AUTHORS
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                                                                                                                                                                                                     AA294641 393 bp mRNA EST 12-NO SWOV3MCA8855K Onchocerca volvulus molting L3 larva cDNA
                                                                                                                                                                                                                                                                                                                                                                                                          20;
 Williams, S.A.,
                                                                           Onchocerca volvulus
                                                                                                                                   AA294641.1
                                                                                                                                                     sequence.
AA294641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0275 row: B column: 24
Seg primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid inserts
                                       Onchocercidae;
                                                       Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                               Onchocerca volvulus.
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                                                                                                                                                                                         (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3C0885 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                 (bases 1 to 393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
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801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g114732114 [gb] AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0275B24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biomedical Polymers Research Bldg.,
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/lab_host="E. coli strain XL10-Gold, T1-resistant,
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                                                                                                                                   GI:2099635
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Lizotte-Waniewski, M.,
                                       Onchocerca.
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1.3e+02;
hes 0;
Laney, S. and Lustigman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 380,
                                                       Spirurida; Filarioidea;
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                                                                                Madimiaria, Landers, Rolling Reinard, R., Werjovski-Almeida,S., Briones,M.R., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW838955 393 bp mrNA EST 18-MAY-2000 CM2-LT0061-180200-094-h05 LT0061 Homo sapiens cDNA, mrNA sequence. AW838955
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
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Contact: Steven A. Williams
Proc. Natl. Ac
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EST.
                                                        Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has I x 1026 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle lizotte Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
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/note="Vector: Lambda Uni-ZAP XR;
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/db_xref="taxon:6282"
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SWOV3WCA761SK Onchocerca volvulus molting L3 larva cDNA
(SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWmL3CO761 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                       Fax: 4135853786
Email: genome@sr
                                                                                                                                                                                        Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Worthampton, MA, 01063, USA Tel: 4135853826
                                                                                                                                                                                                                                                                   Molecular Parasitology
                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                    Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
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Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AA294540
AA294540.1 GI:2099534
EST.
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This sequence was derived from the FAPESP/LICR Human
Project. This entry can be seen in the following URL
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                  Onchocercidae;
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200-094-h05&t3=2000-02-18&t4=1)
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                                                                                                                                                       genome@smith.edu
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/strain-"Kumba, Cameroons"
/db_xref-"taxon:6282"
/clone-"SwmiJ3C0761"
/clone_lib-"Onchocerca volvulus molting L3
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/db_xref="taxon:9606"
                                                                           /organism="Onchocerca volvulus"
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High quality sequence stops: 314 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 714 Std Error: 0.00
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Other_ESTs: yd29all.rl
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 415)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T81898 415 bp mRNA EST 15-MAR
yd29a11.s1 Soares fetal liver spleen 1NFLS Homo sapiens
IMAGE:109628 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                             Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
Insert Size: 714
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H
/clone="IMAGE:109628"
/clone_lib="Soares fet
                                                               /db_xref="taxon:9606"
                                                                                           /db_xref="GDB:465245"
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/dev_stage="molting L3"
/lab_host="XL1-Blue MRF'"
                                                                                                                      /organism="Homo sapiens"
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1997)
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Williams, S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome@smith.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="SWmL3C01534"
/clone_lib="Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Kumba, Cameroons
/db_xref="taxon:6282"
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324 AATTGTGCAAGTGCTCTGGA 343
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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HS_3240_A2_B12_T7 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3240 Col=24 Row=C, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 483.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(206) 616-3887
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a 91 c 107 g 123 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
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/db_xref="taxon:9606"
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100.0%; Pr
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                                         Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                    vg46g09 yl Soares_mammary_gland_NbMMG Mus
IMAGE:864448 5', mRNA sequence.
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20; Conserv
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anai
                                  Mammalia; Eutheria;
1 (bases 1 to 498)
                                                                                                                        EST
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Plate: 42 row: N column: 11
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.989904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U: Tel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
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266990 MARC 3BOV I
                                                                                                       house mouse
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1 (bases 1 to 491)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
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/lab_host="DH10B"
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/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
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Sutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
                                                                                                                    Sequence evaluation of four pooled-tissue normalized bovine libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE602580 505 bp mRNA EST
267845 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF602580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:508536
                                                                          Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF602580.1 GI:11699804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40RP
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a 130 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="faxon:10090"
/clone="IMAGE:864448"
/clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="mammary gland"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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hes 0;
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RESULT 54
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                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
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BG382487.1
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                                                                                       FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 4 TOW: B COLUMN: 11
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                         EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrota
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298398 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                    PCR PRimers
                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                               402 762 4366
402 762 4390
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/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."

155 c 132 g 122 t
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                        Location/Qualifiers
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Pred. No.
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hes 0;
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Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome@smith.edu
Seq primer: pBluescript SK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         College, Northampton, MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Steven A. Williams Molecular Parasitology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onchocercidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOv3MCAM26G12 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 a
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                                                                                                                                 /lab_host="XLI_Blue MFF/"
/lab_host="XLI_Blue MFF/"
/lab_host="XLI_Blue MFF/"
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
/note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2:
Xho I; Filarial nematode parasite of humans. Third-stage
larvae, L3, were isolated from infected black files in
Cameroon (forest strain). The L3 were cultured in 20% FCS
in IMDM+ NCTC 135 and collected after day I, 2, or 3 in
culture. L3 of O. volvulus molt to fourth-stage larvae by
day 5 in culture. mRNA was isolated from approximately
6000 molting larvae (mL3),2000 larvae from day I, 2 or 3
in culture, and converted to double-stranded cDNA using
reverse transcriptase and oligo(dT) followed by RNase H
and DNA pol I. The library was constructed in the lambda
Uni-Zap XR vector and has 1 x 10E6 independent
recombinants and the average insert size is -1200 bp. The
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a 103 c 104 g 162 t
                      slustigm@nybc.org)."
105 c 125 g
                                                                 library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams The library is available from Dr. Sara Lustigman (email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Kumba, Cameroons"
/db_xref="taxon:6282"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SL96MLW-OvmL3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="SWOv3MCAM26G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="molting L3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Onchocerca volvulus molting L3 larva cDNA
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Pred. No.
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                                                                                                                           BI394563 526 bp mRNA EST 06-AUG-2001 pgpln.pk001.110 Normalized Chicken Pituitary/Hypothalamus/Pineal Library Gallus gallus cDNA clone pgpln.pk001.110 5 similar to gi17710042 ref|NP_057930.1| IQ motif containing GTPase activating protein 1; Cdc42-Rac1 effector protein [Mus musculus] sp|Q9UKF1|IQG1_MOUSE RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 gb|AAF60344.1|AF240630_1 (AF240630) IQ motif containing GTPas, mRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Renthomorpha; Acanthopterygii; Percomorpha; Tetraodontidae; Takifugu.

1 (bases 1 to 521)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y., Williams,G. and Brenner,S.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                           Gallus gallus
                                                                      BI394563.1
EST.
                                                                                                   BI394563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-JUN-1998) MRC Centre, Hinxton, Cambridge, biohelp@hgmp.mrc.ac.uk vector: pBluescript II KS
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Takifugu rubripes
                                                            chicken
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/clone="116B21aA4"
120 c 120 g 136 1
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/db_xref="taxon:31033"
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BG351255
BG351255.1
EST.
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Nielsen, K.L, Crookshanks, M., Emmersen, J. and Welinder, K.G.
EST-sequencing of mature potato tuber (Var. Kuras)
Unpublished (2000)
Contact: Karen G. Welinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 526)
Porter,T.E. and Cogburn,L.A.
ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
Library USDA/IFAFS Animal Genome Project
Unpublished (2001)
                                                                                                                                                                                                                              Sohngaardsholmsvej
Tel: +45 96358467
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
20; Conserv
                                                                                                                                                                  Email: kgw@bio.auc.dk
Sequenced from the 5'
                                                                                                                                                                                                             Fax: +45 98141808
                                                                                                                                                                                                                                                                       Aalborg Universitet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Solanum tuberosum
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Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Larry A. Cogburn
University of Delaware
                                                                                                                                                                                                                                                                                           Institut for bioteknologi
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                                                                                                                                             quality
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/organism="Solanum tuberosum"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
/clone_lib="Mature tuber lamb
                                                                                                      Location/Qualifiers
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162 c 151 g 87 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pituitary/Hypothalamus/Pineal Library"
/sex="Male and Female"
/tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
/tissue_type="Embryonic (d12,d14,d19); post-hatch (w1,w3,w5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="E. Coli EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="pgpln.pk001.110"
/clone_lib="Normalized Chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Commercial broiler chicken"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marek,L.F., Paz,M., Darnielle,L., Hanson,N. and Shoemaker,R.C.
BAC End sequences from a soybean genomic library (ISU)
Unpublished (2000)
Contact: Shoemaker Randy C
Agronomy Department
Iowa State University
Ames, IA 5031-1010, USA
Tel: 515 294 1205
Fax: 515 294 2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ221490 541 bp DNA GSS 14-JUN-200 GM_UMb001_125_D12.R UMN Soybean BAC Library (pECSBAC4 ECORI) Glycine max genomic clone Gm_UMb001_125_D12, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ221490 541 bp
Gm_UMb001_125_D12.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Please see as an authority for the mapping/naming: Crégan P.B., Jarvik, A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. K.T.T. VanToai, D.G. Lohnes, J. Chung, and J.E. Specht. 1998a. An integrated genetic linkage map of the soybean genome. Crop Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rcsshoe@iastate.edu
This BAC identified by SSR Satt427. For more information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: BACR or M13R Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39:(In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://genome.cornell.edu/cgi-bin/WebAce/webace?db=soybase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SoyBase at:
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                                                                                                                /note="Vector: pECSBAC4; The UMN BAC library (Danesh et al Theor. Appl. Genet. 96:196, 1998) was constructed using the Eco RI site of pECSBAC4. The library consists of 72, 960 clones with an average insert size of 120 Kb, equal to 7 haploid genome equivalents. Screening of the library done by PCR amplification of DNA pools."
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/note="Vector: Lambd
                                                                                                                                                                                                                                                   /clone="Gm_UMb001_125_D12"
/clone_11b="UMN Soybean BAC Library (pECSBAC4 ECORI)"
/tissue_type="cotyledon leaves"
/dev_stage="cotyledon stage"
                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                       /cultivar="Faribault"
                                                                                                                                                                                                                                                                                                                                                                         /organism="Glycine max"
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                  DB 13; 1
1.3e+02;
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RESULT 61
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AZ298434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org
AQ27,0247 557 bp DNA GSS 03-NOV-1998 HS_2045_Al_G04_MR CIT Approved Human Genomic Sperm Library D Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (Pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea Ch Genetics (lnfo@tresgen.com). BAC end page: http://www.tigr.org/tcb/bac_ends/mouse/bac_end_intro.html Plate: 109 row: A column: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T7
Class: BAC ends.
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Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Sha, Levins, M., Mcgann, S., Tsegaye, G., Geer, K.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10900"
/clone="RPCI-23-109A14"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " a 80 c 76 g 219 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
/lab_host="DH10B"
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Pred. No.
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hes 0;
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BF258009/c
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On Nov 16, 2000
                                                                                                                                                                                                                                                                                               HVSMEf0014H19f Hordeum vulgare seedling root EST library HVcDNA0007 (etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0014H19f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Nat 99380589
                                 Development of a genetically and physically anchored for barley genomics unpublished (2000)
                                                                                            Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Ra,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D.
                                                                                                                                                          Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea;
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                    EST
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Location/Qualifiers
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University of Washington
401 Queen Anne Avenue North,
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
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AQ270247
AQ270247.1 GI:3822842
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                    barley.
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ce Tagged Connector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2045 Col=7 R
/clone_lib="CIT Approved H
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: sperm; Vector: pBeloBAC11; BAC
E-Coli DH10B"
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                3 (2000)
2000 this sequence version replaced gi:11187122
                                                                                                                                                                                                                                                                   GI:13119185
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1.3e+02;
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g,J., Zhao,S., Adams,M.D. and
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306845 MARC 1PIG $
BG385206
BG385206.1 GI:133
                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases cal
v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                              Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                        Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 577)
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Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                                           Plate:
                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                       and -minmatch 12 options
                                                                                                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Hordeum vulgare seedling root
HVCDMA0007 (etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/clone_lib="MARC 1PIG"
               /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                     Location/Qualifiers
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/clone="HVSMEf0014H19f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
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/tissue\_type="pooled"

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Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ570315 577 bp DNA GSS 01-JUN-1999 HS_5352_B1_E02_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-928 Col=3 Row-J, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 577)
                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 577.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.htsc.washington.edu
Plate: 928 row: J column: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High Throughput Sequencing Center 
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jwallace@u.washington.edu
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                                                                                                                     /note-"Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

a 114 c 82 g 130 t 7 others
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/note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
a 200 c 175 g 100 t
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=928 Col=3 Row=J"
/clone_lib="RPCI-11 Human Male BAC Library"
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100.0%; Pr
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                      DB 13; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ987277 580 bp DNA GSS 27-APR-2001
ZM0269J15R MOUSE 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0269J15 R, DNA sequence.
AZ987277
AZ987277.1 GI:13858504
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reill)
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
Plate: 0269 row: J column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 0269 row: J column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lass: plasmid ends
                           169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                   with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance. "

93 g 227 t
                                                                                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                           (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                               polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0269J15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex≖"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'lab_host="E. coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meenen, E., Pedersen, T., Reilly
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Ouery Match Best Local Similarity

0.6%;

Score 20; Pred. No.

DB 13; 1.3e+02;

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SOURCE
ORGANISM
                                                                                                                                                                                                  RESULT 67
AZ802117
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AUTHORS
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                   REFERENCE
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 AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                      2395 tgaaaaacctgaagaagatg 2414
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                                                                                                                                                                                                                                                                      156
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                                                                                                                                                                                                                                                                      TGAAAAACCTGAAGAAGATG 175
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 620)
Dunn,D., Aoyagi,A., E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
                                                                  Mus musculus
                                                                                                                                                  2M0061H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0061H04 F, DNA sequence.
                                                                                                                                                                                   AZ802117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van der Hoeven,R.S., Bezzerides,J., Cho,J., Utterback,T., Hansen
,C.L., Bougri,O., Buell,C.R., Ronning,C.M., Tanksley,S.D. and Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG098273 605 bp mRNA EST 29-JAN-2001
EST462792 sprouting eyes/shoots Solanum tuberosum cDNA clone
cSTC2015 5' sequence, mRNA sequence.
BG098273
                                                                                                                  AZ802117.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of ESTs from potato sprouting eyes/shoots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG098273.1 GI:12588308
                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 605)
                                                                                                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xhol; Various sizes of sprouting eyes (2 mm to 15 mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="sprouting eyes/shoots"
/tlssue_type="sprouting tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4113"
/clone="cSTC2015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Solanum tuberosum"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                  GI:12954536
                                                                                                                                                                                                                                                                                                                                                   0.6%;
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 Barber, M.,
                                 Chordata;
Rodentia;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          119
                                                                                                                                                DNA sequence
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                               Craniata; Vert
Sciurognathi;
 Beacorn, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                                                                                        DB 11;
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                                              Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                    Length 605
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 Duval, B.,
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                                  Muridae;
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                                              Euteleostomi;
                                 Murinae;
                                                                                                                                                                                                                                                                                                                                       0;
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SOURCE
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                                                                                                                                                                                                                                                   CTCAGTTTGGTCCTCAGCAC 199
                                                                                                                                                AI511575 627 bp mRNA EST 16-
SWOvL3CAN30H03SK Onchocerca volvulus infective larva
                                 Onchocerca volvulus
                                                                EST
                                                                                                 mRNA sequence.
AI511575
            Eukaryota;
                                              Onchocerca volvulus.
                                                                                AI511575.1 GI:4417429
                                                                                                                               (SAW94WL-OvL3) Onchocerca volvulus cDNA clone SWOvL3CAN30H03 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rm.
                                                                                                                                                                                                                                                                                                                                                                                                                       167
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             Metazoa; Nematoda; Chromadorea; Spirurida;
Onchocerca.
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2145 ctcagtttggtcctcagcac 2164
                                                                                Local Similarity 100.0%; nes 20; Conservative
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Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Insert Length: 10000 Std Error:
Plate: 0061 row: H column: 04
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Fax: 801 585 7177
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University of Utah
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Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome
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,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasmid inserts
                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gi14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UUGC2M0061H04"
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/strain="C57BL/6J"
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                                                                                                           0.6%; Score 20;
100.0%; Pred. No.
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                                                                                0;
                                                                                Mismatches
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                                                                                1.3e+02;
hes 0;
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Department of Biological Sciences, Clark Science Center,
College, Northampton, MA, 01063, USA
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Williams, S.A., Lu, W
             Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                       Unpublished (2000)
                                                                                                                            plasmid inserts
                                                                                                                                                                                        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                             Mus musculus
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Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams, S.A., Lu, W., Lizotte-Waniewski, M. and Laney, S.J. Genes expressed in infective third stage larvae of Onchocerca
                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sierra Leone"
/db_xref="taxon:6282"
/clone="SWOVL3CAN30H03"
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                                                                                                                                             Genes expressed in microfilaria of Onchocerca volvulus Unpublished (1999) Contact: Steven A. Williams Molecular Parasitology
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20; Conserv
                                                             College, Northampton, Tel: 4135853826
                                                                               Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                               Williams, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW874886 644 bp mRNA EST SWOVMfCAR10G04SK Onchocerca volvulus microfilaria
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Insert Length: 10000 Std Error:
Plate: 0354 row: H column: 14
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                           Onchocercidae; Onchocerca.
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primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (9i14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
                   genome@smith.edu
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/strain="C57BL/6J"
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TITLE
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                                                                                                                                                                                                                                                                                           Email: genome@smith.edu
Seg primer: pBluescript SK.
                                                                                                                                                                                                                                                                                                                                  Fax: 4135853786
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Steven A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes expressed in L2 larvae of Onchocerca volvulus
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/note-"Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: xho I; Filarial nematode parasite of humans mRNA was prepared from approximately 9,000 L2s isolated from infected mosquitoes from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library
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                                                                                                                                                                                                                 /organism="Onchocerca volvulus"
/db_xref="taxon:6282"
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/clone_lib="Onchocerca volvulus L2 larvae cDNA
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/db_xref="taxon:6282"
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/lab_host="XL1-Blue MRF/"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams, S. A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S. Genes expressed in molting L3 larvae of Onchocerca volvulus Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWOV3MCAM07B09SK Onchocerca volvulus molting L3 larva cDNA (SL96MLW-OvmL3) Onchocerca volvulus cDNA clone SWOV3MCAM07B09
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Location/Qualifiers
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larvae, L3, were isolated from infected black files in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of 0. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (mL3),2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 1066 independent recombinants and the average insert size is -1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigm@nybc.org)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="molting L3" /lab_host="XL1-Blue MRF/" /lab_host="XL1-Blue MRF/" /note="Vector: Lambda Un1-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. Third-stage
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/strain="Kumba, Cameroons"
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                            BG310513 660 bp mRNA EST 23-FEB-2 SWOv3MCAM56C02SK Onchocerca volvulus molting L3 larva cDNA
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Unpublished (1999)
Contact: Steven A. Williams
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Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science
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                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 9,000 L2s isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Onchocerca volvulus"
/db_xref="taxon:6282"
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247A05 of
GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith College Department of Biological Sciences Department of Biological Sciences, Clark Science College, Northampton, MA, 01063, USA Tel: 4135853826
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BG310513.1 GI:13112371
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AL186746.1 GT:7824850
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slustigm@nybc.org)."
1 127 c 161 g 185 t
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                                                                                                                                                                                                                        726 bp DNA GSS 12-MAY-2000 nigroviridis genome survey sequence PUC-Ori end of olibrary G from Tetraodon nigroviridis, genomic surve
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/lab_host="XL1-Blue MRF'"
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(SL96MLW-OvmL3)"
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/db_xref="taxon:6282"
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Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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1 (bases 1 to 726)
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/clone="247A05"
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ccagtatcatctgtgaccagc	ggctctgaccaagttcaaattcgtcttcttcctccgtctcag-	totggoaaaggoaagtocaototgotgoagogoattgocatgotot 	Score 59; DB 3; Len Pred. No. 3.3e-07; 0; Mismatches 115;	ion US/08836134A e, Alex E. , Robert G. n, Mani S. Michael alle oh-e Neuronal Apoptosis Inhibitor Protein, Mutations Causative of Spinal Muscular NUMBER: US/08/836,134A 1997-06-20 S: 23 Ver. 2.0	ALIGNMENTS	US-08-644-664B-41 US-09-180-439-1 US-09-180-439-2 US-09-180-439-7 US-09-142-320-8 US-09-142-320-8 US-09-142-320-8 US-09-142-320-8 US-08-851-088-1 US-08-851-088-1 US-08-089-755A-1 US-08-089-755A-1 US-08-089-755A-1 US-08-421-754-1 US-08-421-754-1 US-08-421-754-1 US-08-421-791-1 US-08-421-791-1 US-08-421-791-1 US-08-421-791-1 US-08-421-791-1 US-08-421-791-6 US-09-353-585-1 US-09-353-585-1
س ب ط	tccgtctcag 617	attgccatgctctggg 559                        atagctttctgtggg 1857	gth 5502; Indels 6; Gaps 1;	ın, Gene Sequence and ılar Atrophy		Sequence 41, Appl Sequence 1, Appli Sequence 2, Appli Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 6, Appli

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RESULT 3
PCT-US96-12860-13
$ Sequence 13, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
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US-08-569-749-13
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Best Local Similarity
Matches 123; Conserv
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APPLICANT: Rothe, Mike
APPLICANT: Goeddel, David V
APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                             2109
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                                                                                                                                                                                                                                  2049
                                                                                                                                                                                                                                                                                                                                                                      1869 TGACACATGTCCTATCCTGGATAATCTTCTTGAGGCCAGTGTAATTACAAAACAGG
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CITY: San Francisco
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EDNESS: single
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                                                                                                 Sequence 13, Application US/09212971B
Patent No. 6107041
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Best Local Similarity 46.9
Matches 123; Conservative
                                                                                      GENERAL INFORMATION:
                 APPLICANT: Liston, Peter APPLICANT: Baird, Stephe
                                               APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander
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   APPLICANT:
                                                                                                                                                                                                           2109
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REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
STATE: California
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Tsang,
               Baird, Stephen
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06 AUG 1996
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Pred. No. 0.15;
0; Mismatches 139;
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CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
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Best Local S
Matches 123
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LENGTH: 3151
TYPE: DNA
ORGANISM: Mus musculus
S-09-212-971-13
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08800929A Patent No. 6133437
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                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                 TITLE OF INVENTION: DETECTION AND MODULATION OF TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVITIE OF INVENTION: DISEASE
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APPLICANT:
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Local Similarity 46.98;
nes 123; Conservation
                                                                         COUNTRY: U
ZIP: 02110
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Pratt, Christine
                                                                                                                                                                                                                                                                                                                                         MacKenzie,
                                                                                                                                                                                                                                                                                                                       Liston, Peter
                                                                                                                                                                                                                                                                                                          Baird, Stephen
                                                                                                                                                                                                                                                                                                                                                              Korneluk, Robert G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DETECTION AND MODULATION OF TAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
                                                                                                                                                                                                                                                                                                                                             Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
                                                                                                                                                                                                                                                Sequence 13, Application Patent No. 6300492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
TITLE OF INVENTION: DETECTION AND MODULATIC TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009003 CURRENT APPLICATION NUMBER: US/09/617,053A CURRENT FILING DATE: 2000-07-14 PRIOR APPLICATION NUMBER: US 08/800,929 PRIOR FILING DATE: 1997-02-13
                                                                                                                                                                 APPLICANT: APPLICANT:
                                                                                                                                 APPLICANT:
                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                              2415
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APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 26-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           acttggacgatttggctcagga 311
                                                                                                                                                                                                                                                                                                                                                                                                                                 actatcctctatttcaggacttgaatggacaaagtctttttcatcagacatcagaaggag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGACACATGTCCTTCCTATCCTGGATAATCTTCTTGAGGCCAGTGTAATTACAAAACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACGTTTCAGGCTTGTCATTGGA 2436
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                                                                                                                                 Tsang, Benjamin K
Pratt, Christine
                                                                                                                                                                             Liston,
                                                                                                                                                                   Baird,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3151 base pairs
                                                                                                                                                                                               MacKenzie, Alexander
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                                                                                                                                                                   Stephen
                                                                                                                                                                                  Peter
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                                                                                                 MODULATION DIAGNOSIS #
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                                                                                                   TREATMENT
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PCT-US95-05922A-1
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SEQ ID NO 13
LENGTH: 3151
TYPE: DNA
ORGANISM: Mus musculus
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Best Local Similarity
                                                                              TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HE, ET AL. TITLE OF INVENTION: H
                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1435 BASE PAIRS
                                                                                                 REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
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OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM:
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                                TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/05922A FILING DATE: 11 MAY 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ROSELAND
STATE: NEW JERSEY
                    STRANDEDNESS:
                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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TOPOLOGY:
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EE: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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   LINEAR
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Query Match
Best Local Similarity
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; TOPOLOGY: 1.
; MOLECULE TYPE:
US-08-569-749-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.2
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,781-1989)
                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2589 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goeddel, David V
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1122 AGATGTTTCAGGTCTGTCACTGGA 1145
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1002 TACCATTTTGGTTAAAGGAAATGCTGCGGCCAACATCTTCAAAAACTGTCTAAAAAGAAAT 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             942 GGAACATGATATTAATTAAACAAAAAACACAGATACCTTTACAAGCGAGAGAACTGATTGA 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                              TYPE:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 aatgactgttataaagcaaatcacagatgacctatttgtatggaatgttctgaatcgcga 107
                                                        STRANDEDNESS:
                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT F: 4 Embarcadero Center, Suite 3400 San Francisco
                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
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                                                                                                                                                        (415)398-3249
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                                         linear
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1.2%;

Score 36. Pred. No.

36.8;

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PCT-US96-12860-1
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                                                            Query Match
Best Local Similarity
Matches 122; Conserv
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                                                                                                                                                                                                                              TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TULARIK, INC
TITLE OF INVENTION: INH
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 1607
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BIEZZET, DAVID J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                      TOPOLOGY: 1:
MOLECULE TYPE:
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CITY: San Francisco
STATE: California
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CLASSIFICATION:
                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                aatgactgttataaagcaaatcacagatgacctatttgtatggaatgttctgaatcgcga 107
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4 Embarcadero Center,
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                                                         Score 36.8; DB 5; Pred. No. 1; 0; Mismatches 142;
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RESULT 11
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; NAME/KEY: CDS
; LOCATION: (1160)..(3016)
US-09-205-204-1
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LENGTH: 3532
TYPE: DNA
ORGANISM: Homo s
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Best Local Similarity 46.2%;
Matches 122; Conservative
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CURRENT FILING DATE: 1998-12-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ack
APPLICANT: Lex M. Cowsert
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                                                                     2812 agatgtttcaggtctgtcactgga
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Pred. No. 1.2;
0; Mismatches 142;
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Sequence 7, Application US/09212971B Patent No. 6107041 GENERAL INFORMATION: APPLICANT: KORNELUK, Robert G APPLICANT: MacKenzie, Alexander E

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Best Local Similarity 46.2
Matches 122; Conservative
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LENGTH: 3732
                                                                                                                                                                                                                                                                                                                                                         Patent No. 6133437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND TITLE OF INVENTION: MAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE TITLE OF INVENTION: DISEASE FILE REFERENCE: 07891/009002
                                                                                                                                                                                                                                                                                                                                                                          D8-800-929A-7
equence 7, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Pratt, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liston, Peter APPLICANT: Baird, Stephe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
COMPUTER READABLE FORM
                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & E
                                                                                                                                                                     APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt. Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNO
TITLE OF INVENTION: DISEASE
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                                           COUNTRY:
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                                                                              Boston
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                                                                                                 176 Federal Street
                                               USA
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APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Fratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS /
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-800-929A-7
                                                                                                                                                                                                                                                                                                                US-09-617-053A-7
                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                          Sequence 7, Application US/09617053A Patent No. 6300492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                               APPLICANT: Korneluk, Robert G
                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                3032
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LENGTH: 3732 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2912 TACCATTTTGGTTAAAGGAAATGCTGCGGCCAACATCTTCAAAAACTGTCTAAAAGAAAT 2971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2852 GGAACATGATATTAAACAAAAAAACACAGATACCTTTACAAGCGAGAGAACTGATTGA 2911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 agaagtaaacatcatttgctgcgagaaggtggagcaggatgctgctagaggggatcattca 167
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SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 aatgactgttataaagcaaatcacagatgacctatttgtatggaatgttctgaatcgcga 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 07891/009001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/800,929A FILING DATE: 13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  agacttggacgatttggctcagga 311
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                                                                                                                                                                                                                                                                                                                                                                                                AGATGTTTCAGGTCTGTCACTGGA 3055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                            MacKenzie, Alexander
                                                                                                                                                                                       Liston, Peter
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                                                                                      MODULATION OF DIAGNOSIS AND
                                                                                        IAPS AND
TREATMENT
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                                                                                        OF PROLIFERATIVE
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SEQ ID NO 7

PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0

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Patent No. 591991
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Best Local Similarity 46.2%;
Matches 122; Conservative
                                                                                                                                                                                                                               ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vc
CURRENT APPLICATION DATA:
                                                              APPLICATION NUMBER: US/08/511
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0754
TELECOMMUNICATION INFORMATION:
TELECHIONE: 617/542-5670
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                 INFORMATION FOR SEQ ID NO:
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRITITE OF INVENTION: PROBES, AND DETECTION METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Korneluk, Robert G. APPLICANT: Mackenzie, Alexander APPLICANT: Baird, Stephen
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                            TELEFAX: 01//
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                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                USA
                                                   617/542-8906
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Pred. No. 1.
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Mismatches 142;
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                                                                                                                                                                                                                                                    Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 121; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 29-JAN-1
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1830 TGACTCTACATTGTATAAGAACTTATTTGTGGATAAGAATATGAAGTATATTCCAACAGA 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1710 GGAACATGATATTATAAACAAAAACACAGATACCTTTACAAGCGAGAGAACTGATTGA 1769
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                                                                                                      FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1770 TACCATTTGGGTTAAAGGAAATGCTGCGGCCAACATCTTCAAAAACTGTCTAAAAAGAAAT 1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 agacttggacgatttggctcagga
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                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/484,993B FILING DATE: 09-NOV-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 aatgactgttataaagcaaatcacagatgacctatttgtatggaatgttctgaatcgcga 107
                                                                    NAME: Clough, David W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 :
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: bo
                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
               TELEPHONE:
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312/474-0448
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                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marshall, O'Toole,
                                                                                                                                                                               29-JAN-1993
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                                                                                                                                            07/973,341
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                                                                    36,107
                                                    31745
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South Wacker Drive
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1840 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Felis domesticus
DEVELOPMENTAL STACE: Juvenile
HAPLOTYPE: Diploldy
TISSUE TYPE: OVATY
CELL TYPE: OVATY
EEATURE:
LOCATION: 57..1766
US-08-484-9938-15
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1.1%; Score 34.8; DB 2; Length 1840;
Best Local Similarity 48.5%; Pred. No. 3.3;
Matches 127; Conservative 0; Mismatches 132; Indels 3
1424 GGTGAAAATACTGAAGCGCTTGTAGTAAGATGGAAATGGTGTATCCAGAGCCTTCTGGAC 1365
                                                                           1484 ACAGTGCAGATACACCGGTCCCCTGAGTGCCCACTTTGCCATGGTGTCCACAAAGCTGAA 1425
                                                                                                                                        2745 aaactggagactcacagatacagagattagaattttaggtgcattttttggaaagaaccc 2804
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Search completed: March 25, 2002, 11:40:28 Job time: 3012 sec

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4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn/NA1985.DAT:*

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Copyright (c) 1993 - 2000 Com
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Oligonucleotide D1	AAF58238	22	244	1.3	39.6	44	
	AAF30011	22	32042	•	9	43	
	AAZ09252	20	32042	•	9	42	
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CARD-4S	AAF30003	. 22	3080	•	9	38	
CARD-4S	AAZ09248	20	3080	•	9	37	
Mouse CARD-4L (lon	AAF30006	22	4141	•	۳	36	
Murine CARD-4L cDN	AAZ09251	20	4141	1.3	41.4	35	
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apoptosi	AAT71264	18	6133		59	32	
Neuronal apoptosis	AAT71265	18	6124	1.9	59	31	
	AAA39808	21	5984		. 59	30	
	AAX56272	20	5984		59	29	
	AAX58000	20	5984		59	28	
	AAT71263	18	5502		59	27	
S	AAT30092	17	5502		59	26	
Sis	AAX56273	20	5366		59	25	
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Oligonucleotide D1	582	22	936	3.0	91.8	13	
Oligonucleotide D1	AAF58252	22	936		1	12	

## ALIGNMENTS

AAS03945 Caspase recruitment domain; CARD-12; apoptosis; stress-related pathway; cancer; viral infection; poxvirus; adenovirus; autoimmune disorder; systemic lupus erythematosis; arthritis; neurological disorder; stroke; Alzheimer's disease; amyotrophic lateral sclerosis; haematologic disease; applastic anaemia; myocardial infarction; inflammatory disorder; Crohn's disease; insulin-dependent diabetes; contact dermatitis; psoriasis; graft rejection; bacterial infection; lepromatous leprosy; tuberculosis; ischaemic brain injury; hypoxic brain injury; ss; kidney ischaemia; reperfusion injury; acute bacterial meningitis; excitotoxic brain damage; liver disease. Human caspase recruitment domain 12 (CARD-12) cDNA. 12-SEP-2001 (first entry) WO200130971-A2 Homo sapiens. AAS03945; AAS03945 standard; cDNA; 3133 Location/Qualifiers 36..3110 /\*tag= /product= "Human CARD-12" ВP

26-OCT-2000; 2000WO-US29643

03-MAY-2001.

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1980	gaaacctacattcccagcagggctgtatctttgttcttcaactggaagcaggaattcagg 	1921	Qy
1920 2151	atggcttcatgggaaaaggctgcagaagacacaggtggaatccacatggaagaggcccca 	1861 2092	Оу
1860 2091	cattlgcccaattgtgcaagtgctctggacttcattaaactggacttttatgggggagct	1801 2032	Qy Db
1800 2031	ggtaaaagcttatatatcaactcagggaacatccccgáttacttatttgacttctttgaa 	1741 1972	Qy dd
1740 1971	tatatcaagagagtacatccaaatcagccctgagccaagaatttgaagctttcttt	1681 1912	Qy Db
<b>⊢</b> 8	ctgagcaagaaattctgaaagccataaacatcaattcctttgtagagtgtggcatccat 		Db Qy
55 6		.79	da An
.79	ccaccagggctgttatgaagcacctcgcagcagtgtatcaacacggctgccttctcgga	73	Db Qy
.73	t ccaettatagcagcetgetecggtacacetgtgggtcatetgtggaa 	67	ob Qy
.67	ctcatgagccagaggagtgaccaaggggaatggttacttgcagaaaatggtttccatt 	61	Qy Db
	ttctttcacaagtcattccaggagtacacagcaggacgaagactcagcagtttattgacg 	ப் ப	ДУ
1320 1551	ctgctgacaactgggctcctctgtaaatatacagctcaaaggttcaagccaaagtataaa 		Qy Db
1260 1491	gtgttctcccacaagtttgatttcgaactgcaggatgtgtccagcgtgaatgaggatgtc		Qy Db
1200 1431	gtggctgcaagtgacttcattcggagcctggaccactgtggagacctagctctggagggt 	1141 1372	Qy Db
1140 1371	acgctgttccataccttctatgatctgttgatacagaaaaacaaaacacaaaacataaaggt 	1081 1312	Qy Db
1080 1311	gtggtcatcacttgtgcaatccagatgggtgaaagtgagttccactctcacacaca	1021 1252	Qy Db
1020 1251	ttgttgctccaaattcagaaatccaggtgcttgaggaatctcatgaagacccctctcttt 	961 1192	Qy Db
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ormal apoptosis such as cancer, polypeptide and nucleic acids diagnosing disorders associated , arthritis and Alzheimer's

Disclosure; Fig 2 93pp; English

abnormal level (an increase or a decrease) of apoptotic cell death or abnormal activity of stress-related pathways. The disorders include cancer, viral infections (e.g. caused by poxviruses, alenoviruses), autoimmune disorders (e.g. systemic lupus erythematosis, arthritis), neurological disorders (e.g. Alzhelmer's disease, amyotrophic lateral sclerosis), haematologic diseases (e.g. aplastic anaemia, myocardial infarction, stroke), inflammatory and immune system disorders (e.g. crohn's disease, insulin-dependent diabetes, contact dermatitis, psoriasis, graft rejection), bacterial infections (e.g. tuberculosis, lepromatous leprosy), ischaemic and hypoxic brain injury, kidney The sequence represents a genomic DNA which encodes the human caspase recruitment domain 12 (CARD-12) polypeptide. CARD domains are found in a number of proteins that transmit signals that activate apoptosis and inflammatory pathways in response to stress and other stimuli. Therefore CARD-12 and its corresponding nucleic acid may be used in treatment and diagnosis of patients suffering from disorders associated with an excitotoxic brain damage, bacterial Therefore,

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CC AAH99166 to AAH99904 encode the human proteins given in AAM2525 to CC AAM25963. The proteins can have activities based on the tissues and ccells they are expressed in, such as: antiinflammatory; antirheumatic; CC central nervous system; virucide; anti-HIV; fungicide; antiantic; CC cardiovascular; antianaemic; antiangregant; haemostatic; vulnerary; CC antivice; osteopathic; dermatclogical; antiallergic; antiasthmatic; CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; CC antidiabetic; ortostatic; neuroprotective; antidepressant; nootropic; CC antidiabetic; ortostatic; neuroprotective; antisense therapy and vaccine cytostatics; neuroprotective; antisense therapy and vaccine conding them can be used in gene therapy, antisense therapy and vaccine croding them can be used in gene therapy, antisense therapy and vaccine condinists or antagonists of a protein and for the treatment and diagnosis confidency antipolical architits, septic shock, pancreatitis, cardiac dysfunction, convergathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal confections, autoimmunity, genetic diseases, haematopoietic disorders, costeoporosis, severe combined immunodeficiency, eczema, allergic continitis, asthma, diabetes, cancer, multiple sclerosis, depression, convergical disorders, thrombocytopaenia, neurodegenerative and convergical disorders.
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2000US-0488725.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletion in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                     2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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03-NOV-1999;
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                                                                 microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
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                                             at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                              Claim
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27-SEP-2000;
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26-MAY-2000;
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                                                                                                                                                                                                             (SENP). The present seriom human HeLa cells.
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                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel
                                                                                                                                                                                                          invention relates to human single exon nucleic acid probes present sequence is one such probe. The SENPs are derived HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for gene expression analysis in human cervical cell sample.
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                                                                                                                                                                                                                                                                                                                                                           single exon nucleic acid probes useful ssion in human cervical epithelial cell:
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Best Local Similarity
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                  The present invention relates to single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gexpression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                        Penn
                                                                                                                           Human
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                                                                                                              genome-derived single exon nucleic acid
zing gene expression in human placenta -
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                                                                                                                                                                                                                                                                                                                                                                                                             microarray;
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                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                             antenatal diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   in human placenta
                                                                                                                        probes
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                                                                                                                           useful
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                                                                 (SENP).
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Sequence

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The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the hybridises at high stringency to a nucleic acid expressed in the high breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases

where the probe in the human

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Matches 242;
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                      Claim
                                                                                                                                                                                                           Novel single exon nucleic in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2001;
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                                                                                                                                                                                                                                                                                                                  Hanzel
                                                                                                     invention relates to novel single exon nucleic acid sequence is one such probe. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000GB-0924263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
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                                                                                                                                                                    ID No 4204;
                                                                                                                                                                                                                                                                                                                  DK,
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Pred. No.
                                                                                                                                                                                                                                                                                                                  Rank
                                                                                                                                                                                                                                probe
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. 3.8e-61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
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                                                                                                                                                                                                                                measuring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  include: breast cancer, disorders of development, inflammatory diseases
of the breast, fibrocystic changes, proliferative breast disease and
non-carcinoma tumours.
                                                                                                                                                                                                  30-JAN-2001;
                                                                                                                                                                                                                                                                                        cervical cancer;
                                                                                                                                                                                                                                                                                                   Probe; human;
                                                                                                                                                                                                                                                                                                                        Probe #13523
                                                                                                                                                                                                                                                                                                                                             12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                   Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                   26-MAY-2000;
30-JUN-2000;
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                                                                                      MOLECULAR DYNAMICS
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2000US-0207456.
2000US-068408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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ilarity 100.0%;
Conservative
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                                                                                                           2000GB-0024263
                                                                                                                                                                                                  2001WO-US00670
                                                                                                                                                                                                                                                                                                                       for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                 microarray;
         expression
                                                               DK,
                                                                                                                                                                                                                                                                                                                                                                                         DNA; 220
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                                                                Rank
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. No.
          cervical
                                                                DR;
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3.8e-61;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Human genome-derived single exon nucleic acid probes useful

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3010
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                                                 Novel single exon nucleic in a human breast -
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matory disease; proliferative breast disease;
                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC.
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    SEQ
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2000US-0207456.
2000US-0608408.
2000US-0632368.
2000US-06323686.
2000US-0234687.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3010
         a single
                    Nucleic acids containing electron-transfer group, useful as labels hybridization assays, e.g. for genotyping, allowing repeat analyses
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                                                                                                                                                                                                             01-FEB-2001.
                                                                                                                                                                                                                                                                                                       Electron-transfer group; ETM; mismatch; genotyping;
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17-MAR-2000;
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Matches 6
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RESULT 13 AAF58254 ID AAF582 XX

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                                                                                                                                                                                                                                                                                                                                                                       acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatcl and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Electron-transfer group; gene expression; ss.
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                                                                                                                                                                                                                                                                                                                                                                monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 127; 159pp; English.
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to a composition comprising
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                 gctcaccgcactgatgctgccctggggctgtgacgtgcaaggcagcctgagcagcctgtt
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                                                                 The present invention relates to a composition comprising two nuclei acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                        Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface -
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17-MAR-2000; 2000US-0190259
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                               Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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17-MAR-2000; 2000US-0190259.
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hes 6; Conservative 452; Mismatches 309; Indels
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## SUMMARIES

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CNS016LW CNS007JU AW658668 AI358206 BI391271	BE887277 AW988289 BE544063 BF259322 BG109381 BF257885 BF253881 BF253881 BF253881 AR729528 AQ491970	BE306291 BE64359 AW504276 BG563851 AQ638259 AA669206	AI023795 AZ484615 B58691 AZ762115 AZ614134 AZ362463	AQ112439 BF207840 AW418826 AZ720059 H25984
	BE887277 601508592 AW988289 ug05f04.y BE544063 601069826 BF259322 HVSMEf001 BG109381 602280435 BF257885 HVSMEf001 BF253881 HVSMEf001 BF253881 HVSMEf001 BF253881 HVSMEf001 BF258852 HVSMEf001 BF25881131 601492001 A1729528 BNLGH1135 A0491970 GN616G2 m	BE306291 601103781 BE643259 CT12_B_F0 AW304276 UI-HF-BN0 BG563851 602584655 AQ638259 927P1-17A AA669206 ab93b07.s	A1023795 ox08d03.x A2484615 1M0311P08 B58691 CIT-HSP-201 AZ762115 1M0556N15 AZ614134 1M0442N17 AZ362463 1M0107N03	AQ112439 CIT-HSP-2 BF207840 601862546 AW418826 ha21e11.x AZ720059 RFCI-24-8 H25984 Y156907.r1

## ALIGNMENTS

FEATURES Source	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	RESULT 1 AQ309404/c LOCUS DEFINITION ACCESSION VERSION KEYWOODS
Class: BAC ends. Location/Qualifiers 1552 /organism="Homo sapiens"	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1998) Other_GSSs: CITBI-E1-2528J13.TR Contact: Shaving Theo. William Nierman. Mark Adams	Homo sapiens Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 552) 1 (bases 1 to 552) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.	AQ309404 552 bp DNA GSS 22-DEC-1998 CITBI-E1-2528J13.TF CITBI-E1 Homo sapiens genomic clone 2528J13, DNA sequence. AQ309404 AQ309404.1 GI:4041438 GSS.

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1 (bases 1 to 480)
Olan, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, M., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.
Homo sapiens cDNA GLC clones
                                                                                                                                                    AV719179
AV719179
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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/note="Vector: pBeloBAC11; Site_1: EcoRI;
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121 c 130 g 157 t
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/clone="2528J13"
/clone_lib="CITBI-E1"
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Contact: Zeguang Han
Contact: Aguang Han
Chinese National Human Genome Cent
351 Guo Shoujing Road, Zhangjiang
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801919
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
Location/Qualifiers
                                                                                                                                                                                                                                                                           ttttttgactttagtactaaagaatttctacctgatccagcattagtcagaaaacttagc
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467; Conserv
Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                1M0103H11F Mouse 10kb plasmid UUGC1M clone UUGC1M0103H11 F, DNA sequence.
                                                                      A2360053
                                    house mouse.
                                                           AZ360053.1
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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Pred. No. 4e-113;
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                                                                                                         DNA
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Sciurognathi; Muridae
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                       ataaattctttcacaagtcattccaggagtacacagcaggacgaagactcagcagtttat 1375
                                                                                                                                            atgtcctgctgacaactgggctcctctgtaaatatacagctcaaaggttcaagccaaagt 1315
                                                                                                                                                                                                                          agggtgtgttctcccacaagtttgatttcgaactgcaggatgtgtccagcgtgaatgagg 1255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0103 row: H column: 11
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli xL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oian,B., Wu,T., Huang,Q., Huang,C., Kang,B., Xu,X., Li.N., Peng,Y., Liu,F., Qu,T., Song, Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 371)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
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clone is available at CHGC in
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                                                                                                                                                                    XhoI"
                                                                                                                                                                                               /lab_host="SOLR"
                                                                                                                                                                                                             /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
                                                                                                                                                                                                                                                           /clone-"GLCEQA10"
                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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98.6%;
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Song,H., Cheng,Z.,
1,G., Ren,S., Zhong,
                                                                                                                                                     1 others
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                2731 aagcttgggttgaaaaactggagactcacagatacagagattagaattttaggtgcattt 2790
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364 AAGCTTGGGTTGAAAAACTGGAGACTCACAGATACAGAGATTAGAATTTTAGGTGCATTT 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTCTGCCACAAGCCTCAGGCTGCAAATAAAGAGATGTGCTGGTGTGGCTGGAAGCCTC
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                                                                      al Similarity
342; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI263294 364 bp mRNA
qx57b01.x1 NCI_CGAP_Pan1 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
Seq.primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                               117
                                                                  11.1%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 364.
Location/Qualifiers
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                                                                                                                                                                                            /note-"Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
                                                                                                                                                                                                                                                                /clone="IMAGE:2005417"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                Score 342; DB 10;
; Pred. No. 5.1e-80;
0: Mismatches 0;
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                                                                                                   Length 364;
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Best Local Similarity
Matches 290; Conserv
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2791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG210375 476 bp mRNA EST 21-APR-2001 RST29913 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence. BG210375
                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Athersys, Inc.
3201 Carnegie Ave, Cleveland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E Veloso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Activation of Gene Expression Nat. Biotechnol. 19 (5), 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Creation of Genome-wide Protein Expression Libraries using Random
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                                                                                                                                                                                                  120
                                                                             9.3%;
ilarity 97.6%;
Conservative
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

20 a 99 c 107 g 149 t 1 others
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                                                                             Score 285.8; DB 11;
Pred. No. 4.9e-65;
0; Mismatches 7;
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                                                                                 Indels
                                                                                                                   Length 476;
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Whittington,J.,
Mays,R., Smith,E.,
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Best Local Similarity
Matches 317; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA
Tel: (206) 616-3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17),
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HS_5378_B2_C12_SP6E RPC1
genomic clone Plate=954
                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.htsc.washington.edu
Plate: 954 row: F column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping
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Keller,A., Shaker,R.,
                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 470.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: SP6
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                                                                                                                              142
                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                           BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jwallace@u.washington.edu
                                                                                                                              Ω,
                                                                                                                          Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

101 c 107 g 117 t 3 others
                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone--plate=954 Col=24 Row=F"
/clone_lib-"RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                       /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:5086412
                                  9.2%;
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RPCI-11 Human Male BAC Library Homo sapiens
                   0;
                                 Score 282.8; DB 1
Pred. No. 3.1e-64;
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                     Mismatches
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                                                      DB 13;
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g,J., Zhao,S.,
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                                                  Length
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                   Gaps
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AQ889169
AQ889169.1
GSS:
                                                                                                                                                                                                                                                                        401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ889169 404 bp DNA GSS
HS_2161_B1_A01_T7C CIT Approved Human Genomic
sapiens genomic clone Plate=2161 Col=1 Row=B,
                                                                                                                                                                                                                     Seq primer: T7
Class: BAC ends
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1 (bases 1 to 404)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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                   119
                                                                                                                                                                                  quality sequence stop: 404 Location/Qualifiers
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__Natl. Acad. Sci. U. S. A. 96 (17),
                                                                                                                                                                                                                                                            2161
                   a
                                 /note="Organ: sperm; Vector: pBeloBAC11;
E-Coli DH10B"
                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2161 Col=1
/clone_lib="CIT Approved
                                                                    /sex="male"
                                                                                                                                                                                                                                                            row: B
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Sperm Library D
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Best Local (
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Local Similarity 91.5%;
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                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,
Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Li
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                   Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
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EST.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                     quality sequence stop: 201.
Location/Qualifiers
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             /clone="IMAGE:2918853"
/clone_tib="NCI_CGAP_CML1"
/tissue_type="myeloid cells, 18 prearrangement positive, includes
myeloid blast crisis"
/lab_host="DH10B"
                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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       170;
                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
Other_GSSs: RPCI11-93C9.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ320928 553 bp DNA GSS 06-MAY-1999 RPCI11-93C9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-93C9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                              170
       Conservative
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                                                                                                      /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1:
/PCIII Human Male BAC Library"
a 107 c 114 g 162 t
                                                                                                                                                                                                                 /db_xref="GDB:7535384"
/db_xref="taxon:9606"
/clone="RPCI-11-93C9"
                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                  /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                       location/Qualifiers
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5.5.,
100.0%; P1
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Pred. No.
                      Score 170;
Pred. No.
       Mismatches
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                       3.4e-34;
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                                        DB 13;
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                                                                                                                                               EcoRI; Site_2: EcoRI;
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                                                                                                                                                                        Matches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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     2219
                                                                                                                      2099 tggctggaagcctcagtttggtcctcagcacctgtaagaacatttattctctcatggtgg 2158
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                                                                                                      TGGCTGGAAGCCTTAGTCTGGTCCTCAGCACCTGTAAGAACATTTATTCTCTCATGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
pieter@dejong.med.buffalo.edu, Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berry, K., Granger, D., Suh, E., W
Use of human BAC End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
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RPCI11-78E13.TV RPCI-11
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ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
abor ur 219)
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                    /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                             /db_xref="GDB:7529676"
/db_xref="taxon:9606"
/clone="RPCI-11-78E13"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                    5.1%;
86.1%;
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                                                                                                                                                                      Score 157.2; DB 1
Pred. No. 7.5e-31;
0; Mismatches 28
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                                                                                                                                                                                                        DB 13;
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RESULT 1
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KEYWORDS
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                                                                                                                                                                   Query Match 5.0
Best Local Similarity 85.5
Matches 218; Conservative
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61
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                      totcacacacacacacgotyttccatacottotatgatotyttgatacagaaaacaaa 1125
                                                                                                      agacccctctctttgtggtcatcacttgtgcaatccagatgggt-gaaagtgagttccac 1065
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                                                                                  AGACCCCTCTCTTTGAGGTCATCATTTGTGCAATCTCTATGGACAGAAAGGGAGTTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL2&t2=IL2-MT0180-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 an
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EST.
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IL2-MT0180-181200-276-F03 MT0180 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181200-276-F03&t3=2000-12-18&t4=1)
Seq primer: puc 18 forward
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence start:
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                                                                                                                                                                                                                                                                                                     മ
                                                                                                                                                                                                                                                                                                Inote="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.,716. Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 62 c 56 g 61 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MT0180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
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                                                                                                                                                                                         5.0%;
                                                                                                                                                                     0;
                                                                                                                                                                     Score 153.8; DB 1
Pred. No. 6.2e-30;
0; Mismatches 32
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                                                cattggagagggaatggattacatagtcaagtctctgtcaagtgaaccctgtgaccttga 2468
                                                                                                             agctgaaggcctgaaaaacctgaagaagatgtgtttatttcatttgacccacttgtctga 2408
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                               CATTGGAGAGGGAATGGATTACATAGTCAAGTCTCTGTCAAGTGAACCCTGTGACCTTGA 604
                                                                                             AGCTGAAGGCCTGAAAAACCTGAAGAAGATGTTTTATTTCATTTTGACCCACTTGTCTGA 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
Other_GSSs: CIT-HSP-2372C1.TF
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1 (bases 1 to 630)
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                      HindIII"
                                                                                                                                                                                                                                                                        /sex-"Male"
/cell_type="Sperm"
/note-"Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2372C1"
/clone_lib="CIT-HSP"
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Query Match 4.6%;
Best Local Similarity 91.9%;
                                            3032 atctcagtgttattacaggtgctttttaaactagtaactgct 3072
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ATCTCAGTGTTATTACAGGTGCTTTTAAACTAGTAACTGCT 464
                                                                                                                                                                                             TATCCAAGTTAACTTTTCTGCAAGAAGCTAGGCT - - CTTGGGTGCCATTTGATGATGATG
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Tissue Procurement: ATCC
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Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone=*InAGE::4082074*
/clone=*InAGE::4082074*
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/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
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/db_xref="taxon:9606"
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Search completed: March 25, 2002, 11:37:10 Job time: 2815 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.4%; Score 136; DB 10; Best Local Similarity 100.0%; Pred. No. 3.8e-25; Matches 136; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                     2997
                                                                                                                                                3057 taaactagtaactgct 3072
                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                       449
                                                                                                                                                                                                                                              agctaggcttgttgggtggcaatttgatgatgatgatctcagtgttattacaggtgcttt 3056
                                                                                                                                                                                                                       AGCTAGGCTTGTTGGGTGGCAATTTGATGATGATGTCTCAGTGTTATTACAGGTGCTTT 390
                                                                                                                       TAAACTAGTAACTGCT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 509)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW418826.1 GI:6946758 EST.
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AW418826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW418826 509 bp mRNA EST 09-FEB-2000 ha21e11.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2874380 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 461.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: Kidney; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI (CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatima Bonaldo. "
a 99 c 80 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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